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OM nucleic - nucleic search, using sw model	June 22, 2003, 06:21:26 ; Search time 6392 Seconds (without alignments) 17292.312 Million cell updates/sec	US-09-763-985A-1 score: 3798 :: 1 ccacgcgtccgatggcgacttcaaaaaaaaaaaaa	table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	l: 2054640 segs, 14551402878 residues	Total number of hits satisfying chosen parameters: 4109280
OM nucleic – nu	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number of

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database

Minimum DB seq length: 0 Maximum DB seq length: 200000000

gb_ro:* gb_sts:* gb_sy:* em_ov:* em_pat:* gb_un:* gb_vi:* em_ba:* em_hum: em_fun: gb_ba:* gb_htg:* em_sts: gb_pat:* gb_ph:* em_in:* em_mu:* em_om:* em_or:* em_pl:* em_ro:* #:wo_dp gb_pl:* gb_pr:* gb_in:* GenEmbl:*

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D63879 Human mRNA AF387506 Homo sapi AX268309 Sequence AF17272 Mus muscu AC010206 Homo sapi AC008119 Homo sapi G26688 human STS S Continuation (4 of AC126267 Mus muscu AC12617 Sequence G52164 EST1135 Foe AC126857 Rattus no AC079626 Mus muscu AC126851 Rattus no AC126857 Rattus no AC126857 Rattus no AC079667 Mus muscu 166494 Sequence 14 Z57540 H.saplens C AC128917 Rattus no AC07870 Arabidops AL672124 Mus muscu AC098726 Mus muscu AC08726 Mus muscu AC08726 Mus muscu AC08726 Mus muscu AC18225 Mus muscu AC18225 Mus muscu AL663048 Mouse DNA AC009785 Homo sapi AC101527 Mus muscu AC102097 Mus muscu AC155861 Human DNA AC108444 Mus muscu AC113303 Mus muscu Z55627 H.sapiens C G54201 B13G14/T7 H AB020880 Homo sapi D63879 Human mRNA score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description SUMMARIES AF172722 AC010206 AC008119 AC122224_3 AL663048 AC009785 AC126267 AC128917 HS183C8F AC128917 AB020880 AC079867 **AX268309** 10 01 DB 99.3 3788 96.3 3660 95.1 3644 56.7 3586 27.8 171523 27.8 171523 27.8 171523 8.9 86096 8.9 319737 8.1 94682 6.1 314 3.5 207933 3.2 180819 3.0 138810 2.5 7218 2.4 94682 2.3 94682 Length 180819 1.8 197346 1.8 195690 1.7 215219 1.7 234817 1.7 179145 1.7 198228 1.7 168528 1.7 168528 1.7 168528 Query Match 112.4 97.8 95.6 90.6 2886 2154.2 1056.4 1056.4 602 603 7. 603 7 Score 9977 O

ALIGNMENTS

AC122186 Mus muscu AL844566 Mus muscu AC073495 Mus muscu

Y15251 Drosophila AY061395 Drosophil AC118889 Rattus no

DM4 FRNPN AC118889

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AL645740 Mouse DNA AL603745 Mus muscu AL844169 Mus muscu

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AB020880 3788 bp mRNA linear PRI 03-JUN-1999 Homo sapiens mRNA for squamous cell carcinoma antigen SART-3, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 3788)
Itoh.K., Yang,D., Sasatomi,T., Nakao,M., Shichijo,S., Takasu,H., Matsumoto,H., Mori,K. and Yamana,H. AB020880.1 GI:4996281 squamous cell carcinoma antigen SART-3. Homo sapiens squamous cell carcinoma cell_line:KE4 cDNA to mRNA. Homo sapiens complete cds. AB020880 RESULT 1 AB020880 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

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                                    Itoh, K., Yang, D., Sastomi, P., Nakao, M., Shichijo, S., Takasu, H., Matsumoto, H., Mori, K. and Yamana, H.

Direct Submission
Submitsed (07-DEC-1998) Kyogo Itoh, Kurume University, Department of Immunology; 67 Asahi-machi, Kurume, Fukuoka 830-0011, Japan (E-mail:kyogo@med.kurume-u.ac.jp, Tel:81-942-35-3311, Fax:81-342-31-7699)
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Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
Direct Submission

Birect Submission

1532-3, Yana, Kisarazu, Chiba 292-0812, Japan

(B-mall:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
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	361 CTGCTCAGGCTGGAAGGGACCTTACCAAGGTGAGGATGGCCCGCCAGAAGATGAGAA 420 432 ATCTTCCCTTGACTGAAGACCTCGCTGGAGGGTGGCTCCATGACGACATTACATGACATTACATGACATTACATGACATTACATGACATTACATTACATGACATTACATTACATGACATTACATTACATGACATTACATTACATGACATTACATTACATGACATTACATTACATGACATTACATTACATGACATTACATTACATGACATTACATACA	ATTGCCCTAACATTGGCTAGAGTATGGCCAGTACTCAGTTGGTGGGATTGGTCAGAAA	ATGACCAAAGGACTCGCCCTCTGGGAGGCTTACCGAGAGTTTGAAAGTGCGGATGTGGGAA 7 [792 GARTAGGAGGCCARATTGGAGGATAGGAGGAGGAGGATACCAGGGTCA 851 11111111111111111111111111111111111		1032 TGCCTTGTCCCAGACTTATGGATCCGTTACAGTCAGTACCTAGATCGACAACTGAAAGTA 1091	1152 TTATGGAGTCGGTACCTCTTGGCCATGGAGACATGGAGTTGATCATCAAGTAATTTCT 1211 1141 TTATGGAGTCGGTACCTCTTGGCCATGGAGACATGGAGTTGATCATCAAGTAATTTCT 1210 11212 GTAACCTTCGAGAAAGCTTTGAATGCCGGCTTCATCCAGGCCACTGATTATGTGGAGATT 1271 1201 GTAACCTTCGAGAAAGCTTTGAATGCCGGCTTCATCCAGGCCACTGATTATGTGGAGATT 1271 1201 GTAACCTTCGAGAAAGCTTTGAATGCCGGCTTCATCCAGGCCACTGATTATGTGGAGATT 1260 1272 TGGCAGGCATACCTGATTACCTGAGGAGAAGGGTTCATTCA
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2412 CACAAGCTGTTCATCTCAGGCCTGCTTTCTCCTGTACTAAAGAGGAACTAGAAGAAATC [Qy 2592 ATGGACGCATGACTATCAAAGAGAACATCATCAAAGTGGCAATCAGCAACCTCCTCAG 2651 Db 2581 ATGGACGCATGACTATCAAAGAGAACTCATCAAAGTGGCAACCTCTCAG 2640 Db 2652 AGGAAAGTTCCAAGAAGCACAGAAGCCACCAGGAAGTGCCAATCCTTTTGCCG 2711 Db 2641 AGGAAAGTTCCAAGAAGCCACAGGAAGCCACCAGGTGGCCCCATGCTTTTGCCG 2710 Qy 2712 CAGCATACGGAGGGGAAGGAAGCCACACACACACACTCTCTCT	RESULT 5 AF17272 LOCUS LOCUS LOCUS DEFINITION MUS musculus tumor-rejection antigen SART3 (Sart3) mRNA, complete ACCESSION VERSION VERSION AF17272 AF1727 AF
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David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D., Forcum-Transey, J., Frantz, P., Ganeel, R., Gorrell, J. H., Gorrell, L.L., Guevara, W., Harris, R., Hernandez, J., Hodgson, A., Hoques, M., Harris, R., Hernandez, J., Hodgson, A., Hoques, M., Jones, M., Kelly, S., Kneitz, S., Kondejewski, N., Kong, Y., Kovar, C., Lau, S., Leal, B., Lee, E., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R., Lu, J., Lu, J., Lu, Liu, J., Liu, M., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Merscher, S., Miller, A., Montgomery, K.T., Morgan, M., Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, N., Olwal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pul. L., Quiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Shim, C., Simon, M., Sparks, A., Stamps, A., Stamps, A., Sucgang, R., Tabor, P., Tabor, P., Weinstock, G., Weinstock, G., Weinstock, G., Weinstock, G., Weinstock, G., Khang, A.M., Yang, R., Yu, W., Zhou, X., Kreherlapati, R., Nelson, D. and Gibbs, R. Direct Submission
Submitted (15-SEP-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 171523)
Worley, K.C. Unpublished 2 (bases 1 to 171523) Worley, K.C. Direct Submission Gibbs, R. AUTHORS TITLE JOURNAL REFERENCE TITLE JOURNAL JOURNAL AUTHORS REFERENCE

Submitted (08-DEC-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases I to 171523) Worley, K.C.

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

Direct Submission

Submitted (313-MAR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 8, 1999 this sequence version replaced gi:6513881.

INFORMATION: http://www.ngsc.bcm.tmc.edu/ or email

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets.stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

QUALSTAT-REPORT------

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Distribution of Quality < 40 Bases

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qxfo Version: 1.01 --- Summary Statistics

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Contig length: Phrap values in estimate: Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40: Number of consensus changing edits: Number of N's in consensus:	Position Original+Context Bdited+Context 1245	Ouery Match 27.8%; Score 1056.4; DB 9; Length 171523; Best Local Similarity 99.9%; Pred. No. 2.2e-245; Length 171523; Matches 1057; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Oy 2726 GadGGGAAGGAAGGAAGCTGTCTCTACTGCCTCGCCCTGCCCGCGCCCCAGGGG 2785 111111111111111111111111111111111111

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Submitted (24-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 17315)
                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (28-SEP-1999) Human Genome Sequencing Center, Department
Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 173153)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 173153)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON Sep 28, 1999 this sequence version replaced gi:5776564.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
Scherer, S., Shah, E., Shen, H., Shim, C., Simon, M., Sparks, A., Stamps, A., Sucgang, R., Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo.O., Wahbah, M., Watlington, S., Wainstock, G., Weinstock, T.R., Williamson, A., Worley, K., Wren, J., Wiensford, G., Xhang, A.M., Yang, R., Yu, W., Zhou, X., Kucherlapati, R., Nelson, D. and Gibbs, R.
                                                                                                                                                                                              (bases 1 to 173153)
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Local mapping error. See the property of the p identical matches are annotated as similar. SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage. QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

QUALSTAT-REPORT------

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--- Summary Statistics

Contig lengtl Phrap values Average errol Fraction of I Number of con	ength: lues in estimate: error rate (BCM-Phrap estimate): of Phrap values less than 40 : f consensus changing edits: f N's in consensus :	173153 172401 0.00022158 0.0281147 43
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72	n)acnacca	(c)ac
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2674	(a)	9
74	3	(C)
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4 4	tttocactat(n)accacct	tttccactc)accaccacct
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
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Tel: 617 252 1900
Fax: 617 252 1902
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Primer B: ATCTCAGGACACCACATCCTG
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1 (bases 1 to 771)
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27.8%; Score 1056.4; DB 9; Length 173153;
Best Local Similarity 99.9%; Pred. No. 2.2e-245;
Matches 1057; Conservative 0; Mismatches 1; Indels 0; G.
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complement(3383. .3426)
/rpt_family="MLTIK"
complement(3611. .3732)
/rpt_family="MIR"
4373. .4663
                                                                              /organism="Homo sapiens'
/db_xref="taxon:9606"
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/rpt_family="MLT1K"
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/rpt_family="LTR16C"
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/db_xref="taxon:9606"
/map="518.1 cR from top of Chr12 linkage group"
32. 252
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Location/Qualifiers
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99.9%;
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KCl: 50 mM
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pH: 9.3
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 ATGCAAACTTCAATTCTCCCCATTTAGCTTTAATTAAACTGACGTTCTCTTC
            Indels
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                                                                                                                                                                                                       Score 338.2; DB 2;
Pred. No. 8e-71;
0; Mismatches 578;
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	AC126267 Mus musculu		HTG; HTGS_F house mouse Mus musculu	Mammalia; E 1 (bases 1 McPherson, J		Submitted (Parkway, St	Center: Was Center code Web site:ht Contact: su	Center proj	Sequencing Sequencing Chemistry: Chemistry:	Assembly pr Consensus of Consensus of Consensus of	* NOTE: Thi * consists * is not kn	* arbitrary * runs of N * This reco	* be preser * 1 * 1317 * 1417	* 3097 * 3197 * 8085 * 8185	* 14193 * 14293 * 18776 * 18876	* 27061 * 27161 * 36166 * 36266	* 42//1 * 42871 * 83819 * 83919	* 109450 * 109550 * 176792 * 176892 * 219805
AC126267/c	LOCUS	ACCESSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	JOURNAL JOURNAL REFERENCE AUTHORS TITLE	JOURNAL												
	61382	773 GTTGGCGATCCCACTCTATGATATGGAGGCCACATTTGCAGAGTATGAAGAATGGTCAGA 832 	833 AGACCCAATACCAGAGTCAGTAATTCAGAACTATAACAAAGCACTACAGCAGTGGACAA 892 	893 ATATAAACCTATGAAGAAGCACTGTTGCAGGCAGAGGCACCAAGGCTGGCAGAATATCA	953 AGCATATATCGATTTTGAGATGAAAATTGGCGATCCTCGCCATCAGTTGATTGA	1013 GCGCGCCTGGTCGAGACTGCCTTGTCCCAGACTTATGGATCCGTTACAGTCAGT	1073 AGATCGACAACTGAAAGTAAAGGATTTGGTTTTATCTGTACATAACCGCGCTATTAG 1129 	1130 AAACTGCCCTGGACAGTTGCCTTATGGAGTCGGTACCTCTTGGCCATGGAGACATGG 1189 	1190 AGTTGATCATCAAGTAATTTCTGTAACCTTCGAGAAAGCTTTGAATGCCGGCTTCATCCA 1249 	1250 GGCCACTGATTATGTGGAGATTTGGCAGGCATACCTTGATTACCTGAGGAGGGTTGA 1309 	1310 TITCAAACAAGACTCCAGTAAAGAGCTGGAGAGTTGAGGGCCGCCTTTACTCGTGCCIT 1369 	1370 GGAGTATCTGAAGCAGGAGGTGGAAGAGCGTTTCAATGAGAGTGGTGAACCTGCGT 1429 	1430 GATTATGCAGAACTGGGCTAGGATTGAGGCTCGACTGCGCAATAACATGCAGAAAGCTCG 1489 	1490 GGAACTCTGGGATAGCATCATGACCAGGGAAATGCCAAGTACGCCAACATGTGGCTAGA 1549	1550 GTATTACAACCTGGAAAGAGCTCATGGTGACACCCAGCACGGGAAGGCTCTGCACCG 1609 	1610 GGCCGTCCAGTGCACCAGACTACCCAGAGCACGTCTGCGAAGTGTTACTCACCATGGA 1669	1670 GAGGACAGAAGGTTCTTTAGAAGATTGGGATATAGCTGTTCAGAAAACTGAAACCCGATT 1729 	1730 AGCTCGTGTCAATGAGGAAGGAAGG 1758 1 111 1111 1111 1 1111111 60422 AACTCATGAGTTGATAATGAAGG 60394
i	a a	č a	δ d	ò a	oy d	δο q <u>α</u>	Qy Dp	oy B	QY	QY Db	VQ QQ	QV Db	oy D	Qy Db	Qy Db	Qy Db	Oy Db	å å

319737 bp DNA linear HTG 04-JUL-2002 us chromosome UNK clone RP23-191M12, WORKING DRAFT 14 unordered pieces. J.D. and Waterston, R.H. bmission (04-JUL-2002) Genome Sequencing Center, 4444 Forest Park St. Louis, MO 63108, USA Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. his is a 'working draft' sequence. It currently s of 14 contigs. The true order of the pieces known and their order in this sequence record is ry. Gaps between the contigs are represented as N, but the exact sizes of the gaps are unknown. cord will be updated with the finished sequence as it is available and the accession number will de: WUGSC http://genome.wustl.edu/gsc/index.shtml submissions@watson.wustl.edu ---- Project Information oject name: M_BA0191M12 shington University Genome Sequencing Center 18875: gap of unknown length 27060: contig of 8185 bp in length 27160: gap of unknown length 36165: contig of 9005 bp in length 36165: contig of 9005 bp in length 36265: gap of unknown length 42870: contig of 6505 bp in length 42870: gap of unknown length 83118: contig of 40948 bp in length 83118: contig of 40948 bp in length 109449: contig of 25531 bp in length 106549: gap of unknown length 176791: contig of 67242 bp in length 176891: gap of unknown length 318952: contig of 99048 bp in length 318952: contig of 99048 bp in length 318952: contig of gap of unknown length ing vector: M13; 0% in a vector: M13; 0% in a vector: M13; 0% in a vector: M13; 0% of reads ry: Dye-primer ET: 0% of reads ry: Dye-terminator B1g Dye; 100% of reads y program: Phrap; version 0.990319 us quality: 309491 bases at least Q40 us quality: 313307 bases at least Q20 6: contig of 1316 bp in length
6: gap of unknown length
6: contig of 1680 bp in length
6: gap of unknown length
4: contig of 4888 bp in length
4: gap of unknown length
5: contig of 6008 bp in length
5: gap of unknown length
6: gap of unknown length
7: contig of 4483 bp in length PHASE1; HTGS_DRAFT; HTGS_FULLTOP. 1 to 319737) J.D. and Waterston, R.H. ----- Genome Center GI:21693979 1 to 319737) erved. 219905 318953

451 AGCTCTGGCTGGAGTGGCTGCATGACGAGATCAGCATGGCCCAGGATGGCCTGGACAGAG 510) 511 AGCACGTGTATGACCTCTTTGAGAAAGCCGTGAAGGATTACATTTGTCCTAACATTTGGC 570	571 TAGAGTATGGCCAGTACTCAGTTGGTGGGATTGGTCAGAAAGGTGCCTTGAGAAAG 627 190147 HALLILL III III III III III III III IIII III II	628TTCGCTCGTGTTTGAAAGGCCTCT	199088 ITTIGITGITGITGITGITGITGITGITGITTTTTTTTCTGGGGGGTTAAGAGAAAGITGI 199029 7 653 CICGICIGITGGTITACAIATGACCAAAGGACTCGCCCCTCTGGGAGGCTTACCGAGAGIT 712	199028 GTCATTCCTTGATTTACAFATGTCCAAGTACAGTGCCATCTGGGAGGTTTACTGTGGAGAC	713 TGAAAGTGCGATTGTGGAAGCTGCTCGGCTTGAGAAAGTCCACAGTCTTTCCGGCGACA 772	773 GTTGGCGATCCCACTCTATGATATGGAGGCCACATTTGCAGAGTATGAAGAATGGTCAGA 832	** 833 AGACCCAATACCAGAGTCAGTAATTCAGAACTATAACAAAGCACTACAGCAGCTGGAGAA 892	893 ATATAAACCCTATGAAGAAGCACTGTTGCAGGCAGGGAGCACCAAGGCTGGCAGAATATCA 952 1 1 1 1 1 1 1 1 1	953 AGCATATATCGATTTTGAGATGAAAATTGGCGATCCTGCTTGCGTTCAGTTGATCTTTGA 1012	1013 GCGCCCCTGGTCGAGAACTGCCTTGTCCCAGACTTATGGATCGGTTACAGTCAGT	1073 AGATCGACAACTGAAAGGATTTGGTTTTATCTGTACATAACCGCGCTATTAG 1129 111	1130 AAACTGCCCTGGACAGTTGCCTTATGGAGTCGGTACCTCTTGGCCATGGAGACATGG 1189	1190 AGTIGATCATCAAGTAATTTCTGTAACCTTCGAGAAAGCTTTGAATGCCGGCTTCATCCA 1249	1250 GGCCACTGATTATGTGGAGATTTGGCAGCCATACCTTGATTACCTGAGGAAGGGTTGA 1309	1310 TTTCAAACAAGACTCCAGTAAAGAGCTGGAGGAGTTGAGGCCGCCTTTACTCGTGCCTT 1369 	1370 GGAGTATCTGAAGCAGGAGGTGGAAGAGCGTTCAATGAGAGGTGGTGATCCAAGCTGCGT 1429 	1430 GATTATGCAGAACTGGGCTAGGATTGAGGCTCGACTGTGCAATAACATGCAGAAAGCTCG 1489
Oy Op	QQ QQ	oy d	70 YO	da VQ	다 선	Qy Db	ζς QΩ	QY Db	da Oy	QQ QQ	da da	Qy Db	Qy Db	QQ Dp	QY	QY DP	Qy	Oy Db
* 319053 319737: contig of 685 bp in length. FEATURES Location/Qualifiers source //organism=Mus musculus"	/u_Are:- cakou:10050 /chromosome="UN" /clone="RP23-191M12" nisc_feature 11316	/loce="assemply_name:Contig13" misc_feature 1417 .3096 //note="assembly_name:Contig14" misc_feature 3197 8084	/note=" 8185 /note="	misc_feature 14293. 18775 //note="assembly_name:Contig17" misc_feature 18876. 27060	/note="assembly_name:Contig18" misc_feature 27161. :36165 /note="assembly_name:Contig18"	misc_feature 36266. 42770 misc_feature 42871. 83818	//octe-assembly_name:Contig1" misc_feature 83919. 109449 misc_feature 109550. 176791	/note="assembly_name:Contig23" nisc_feature /176892, .219804 nisc_feature 219905, .318952	/note="assembly_name:Contig25" misc_feature 319053. 319753. 31971y_name:Contig8" Anote="assembly_name:Contig8" DASE COUNT 91273 a 65131 c 64726 g 97306 t 1301 others	y Match 8.9%; Score 338.2; DB 2; Length 319737; Local Similarity 59.5%; Pred: No. 8.7e-71; American Pred: No. 8.7e-71; 162. Constitution of the 1088.	CONSCIPCTOR CTGCGGCCGAAACCTCGC CAGCAGGTGCAACCCAA	77 TGACGGGAGGGGGGGTTAAGGCGGCTAGGACAAGGAGAAAGGTGTTATCGCGGGC 19672 GGAAAAAGGGGAAATGCAGTTAAGCGGCTAGGATGAAGGAAG	137 TGTGGCGCTGCGACATACAAGACCATGGGGCCAGCGGGGTGGGATCAGCAGGAGGGGT 196	OY 197 GAGGGAGAGGGATGAGTAC GCCATGGCTTCCTCCGCGGAGAGTCCCCGG 253 Db 199557 AAGTGAGAAATGGGGATGAGATGTCTTTGACTTCTTGGAGGACTTCTTTTG 19498	GGAGTACGAGTGGGAATATGACGAAGAGGAGGAGAAAACCAGC297 	Qy 298	391	392 GCTTACCAAGGTGAGGGATGCCCGCCAGAAGATGTGAATCTTTCCCTTGACTGAAGGTGAAGTGAATCTTTCCCTTGACTGAAGGTGAGTGA

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(see http://www.hgsc.bcm.tmc.ed/docs/Genbank_Caraft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                            Direct Submission
Submitted (24-011-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
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Contact: hgsc-help@bcm.tmc.edu
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Babrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Babrooks, J.C., Edwin, J., Benton, J., Blange, K., Blankehurg K., Boonin, D., Bouck, J., Bowle, S., Birkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavacos, S.R., Chacko, J., Chavaz, D., Chen, G., Chen, G., Chen, G., Choyle, M.D., Dathorne, S.R., David, R., Davila, M., Cho, J., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M., Davis, C., Day-Carroll, L., Dederich, D.A., David, R., Davis, C., Day-Carroll, L., Dederich, D.A., David, R., Davis, C., Day-Carroll, L., Dederich, D.A., David, R., David, M., Gancia, J., Garcia, A., Garner, T., Garza, N., Harnandez, J., Harris, K., Hart, M., Halve, S., Hane, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jay, M., Marlin, B., Jacobson, B., Jia, Y., Johnson, R., Jay, M., Martindale, A., Martine, E., Mastine, J., Lu, X., Ludier, A., Ludier, R., Ludier, R., Martindale, M., Martin, R., Marting, E., Marting, R., Martin, R., Mapua, P., Martin, R., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mayue, P., Martin, R., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mayue, R., Marting, R., Pull, L., Chora, S., Soott, G., Shen, H., Shooshtari, N., Sisson, I., Rives, M., Rei, S., Warten, S., Soott, G., Shen, H., Shooshtari, N., Sisson, I., Rives, M., Satek, A., Rabor, P., Wardon, S., Warten, S., Soott, G., Shen, H., Shooshtari, N., Shooshtari, N., Vinger, N., Wang, S., Warten, R., Wardhens, S., Warten, R., Wardhens, S., Warten, R., Wardhens, S., Warten, R., Wardhens, S., Warten, R.,
                                               P4ths norvegicus clone CH230-337D11, *** SEQUENCING IN PROGRESS ***, 64 unordered pieces.
                                                                                                                                                                               1610 GGCCGTCCAGTGCACCAGTGACTACCCAGAGCACGTCTGCGAAGTGTTACTCACCATGGA 1669
                      1490 GGAACTCTGGGATAGCATCATGACCAGAGGAAATGCCCAAGTACGCCAACATGTGGCTAGA 1549
                                                                                                  1550 GTATTACAACCTGGAAAGAGCTCATGGTGACACCCCAGCACTGCCGGAAGGCTCTGCACCG 1609
                                                                                                                                                                                                                                                             GAGGACAGAAGGTTCTTTAGAAGATTGGGATATAGCTGTTCAGAAAACTGAAACCCGATT 1729
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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gap of unknown length
contig of 1323 bp in length
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contig of 1033 bp in length
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contig of 1493 bp in length
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                            Length 94682;
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Human polynucleotides and polypeptides encoded thereby
Patent: WO 0190366-A 5259 29-NOV-2001;
Curagen Corporation (US)
Location/Qualifiers
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                                                                                     Indels
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                                                                      Pred. No. 4.8e-63;
0; Mismatches 88;
                                                             DB 2;
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82.7%; Pred. No. 1.6e-45;
iive 0; Mismatches 56;
                                                                                                                                                                                                                         DNA
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Sequence 5259 from Patent WO0190366.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 82 c 104 g 68
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                                                             Score 306.2;
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AX312274.1 GI:17897367
80160:
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81636:
81736:
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ilarity 80.3%;
Conservative
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Best Local Similarity 82.7
Matches 267; Conservative
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Best Local Similarity
Matches 372; Conserv
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3562 IGACC----TGTGTTGTCTAAACATGAGTTTCAGCCCTTTGGTTTTGTTT-AATACCATG 3616
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1e 53g8, forward
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1 (bases 1 to 218)
MacDonald,M., Huckle,E., Wilkinson,P. and Micklem,G.
Direct Submission
Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="60-day foetus"
/clone_lib="Foetal cDNA library directionally cloned in
/uliap_xR vector"
/note="Vector: Bluescript; V-type: phagemid; A whole
foetus was used a source of RNA in the construction of a
Stratagene Unizap xR directional library. The phagemid
Bluescript was excised from the virus vector and used as
template for sequencing reactions from the 3' end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                 PCR works in the horse and not mouse for specific use in RH panel
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Pred. No. 6e-36;
0; Mismatches 40;
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                                                                                              /organism="Equus caballus"
/db_xref="taxon:9796"
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read cpg53g8.ftlb.
255627
255627 1 GI:1021668
CpG island; genomic Msel fragment.
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54 g
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/gene="SART1"
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/gene="SART1"
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84.0%;
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   Triton X-100
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                                                                                                                                                                                                                                                                                                                                                                   GG2164 1135 Foetal cDNA library directionally cloned in Unizap XR vector Equus caballus STS cDNA 3', sequence tagged site.
                                                                                                                         1289
                                                                                                                                                                                      1170 TTGGCCATGGAGACATGGAGTTGATCATCAAGTAATTTCTGTAACCTTCGAGAAAGCT 1229
                                                                                              180
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Barandon, K., Thomas, S. and Bell, K.
Development of equine expressed sequence tags for use in radiation hybrid mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equus caballus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                  121 CTGAGTGCCGGCTTCATCCAGGCCACTGACTATGTGGAGATCTGGCAGGTGTACCTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 degrees C for 3.00 minute 60 degrees C for 1.00 minute 72 degrees for 1.00 minute. 95 degrees C for 0.45 minute 60 degrees C for 1.00 minute. 72 degrees for 1.00 minute. 95 degrees C for 1.00 minute. 72 degrees C for 1.00 minute 72 degrees for 10.00 minute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Richard Brandon
Australian Equine Blood Typing Research Laboratory
University of Queensland
YI Lucia, Brisbane, Queensland, 4072, Australia
Tel: 61733658501
Fax: 61733654899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: brandon@plpk.uq.edu.au
Primer a: GTGACACTTGTTTTATAGCAATTCTG
Primer B: CAAAATACATCCATATTTGAATGC
STS size: 241
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100ng
each 0.5 uM
each 200 uM
0.02 units/ul
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16.6 mM
67 mM
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Total Vol:
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MgC12:
(NH4)SO4:
Tris-HC1:
Gelatin:
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STS size: 201

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 AAGACCATGGGGCCAGCGTGGGATCAGCAGGAGGAAGGCGTGAGCGAGGGGATGGGGGAT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk 2 (bases 1 to 218) Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P. Purification of CpG islands using a methylated DNA binding column Nat. Genet. 6 (3), 236-244 (1994) 94282070
                                                                                                                         Vector: pGEM-5zf(-)
Lones are available from the UK MRC Human Genome Mapping Project
Resource Centre, Hinzton, Cambridgeshire CB10 1RQ, UK. See URL:
http://www.hgmp.mrc.ac.uk/ for details
or contact: biohalp@hgmp.mrc.ac.uk.

I contact: biohalp@hgmp.mrc.ac.uk.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TAAGGCGGCTAGGACAAGGTAGTAAAGGTGTTATCGCGGGCTGTGGCCGCTGCGACATAC
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A Sequence Ready Map of Human Chromosome 12 (1999)
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Pred. No. 3.3e-34;
0; Mismatches 4;
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a 43 c 85 g
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Primer A: AGCCTGTCCACGTTTCTCTC
Primer B: GCTCTTTTCCGTTGTTCAGC
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96.8%;
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Best Local Similarity 96.8
Matches 211; Conservative
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(http://bacpac.med.buffalo.edu/) Maps between AFM3O4wg5 and
AFM116xb8.
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32. .32
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Polymerization:
PCR Cycles:
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primer_bind
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 18, 2003, 13:47:23; Search time 46 Seconds (without alignments) 4313.552 Million cell updates/sec Run on:

US-09-763-985A-2 Title: Perfect score:

1 MATAAETSASEPEAESKAGP......AATEAPKMSNADFAKLFLRK 963 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 segs, 206047115 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

sp_fung1:*
sp_human:*
sp_invertebrate:* sp_mhc:*
sp_organelle:*
sp_phage:* sp_archea:*. sp_bacteria:* sp_rodent:* sp_mammal:* sp_plant:* sp_virus:* SPTREMBL_21:* 11122::1142::1152::115

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp_rvirus:*
sp_bacteriap:* sp_archeap:*

sp_unclassified:*

sp_vertebrate:*

SUMMARIES

					CELTAINING	
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Result		Query	Query			
No.	Score	Match	Length	DB	ΩI	Description
1	4994	100.0	963	4	915020	O15020 homo sapien
2	4379.5	87.7	962	11	09JL18	09ili8 mus musculu
3	1812	36.3	364	4	096795	096195 homo sapien
4	902	18.1	816	10	616880	08s9i9 arabidopsis
5	864	17.3	836	S	017430	017430 caenorhabdi
9	823	16.5	768	10	C9STW7	09stw7 arabidopsis
7	506.5	10.1	1014	e	Q9USY2	Ogusy2 schizosacch
8	425	8.5	941	Ŋ	Q9W4D2	09w4d2 drosophila
6	420	8.4	943	2	018352	018352 drosophila
10	349	7.0	826	٣	001491	001491 ophiostoma
11	293.5	5.9	705	13	006459	006459 xenopus lae
12	280	5.6	744	2	016376	O16376 caenorhabdi
. 13	272	5.4	1305	S	Q9NFE2	O9nfe2 drosophila
14	263.5	5.3	665	10	Q9FJ37	09fi37 arabidopsis
15	252.5	5.1	715	11	0902X1	09qzxl rattus norv
16	249.5	5.0	707	11	Q99K50	099k50 mus musculu

0911h8 arabidopsis 09fvq1 arabidopsis 09byd tarosophila 09byd homo sapien 09ffm3 arabidopsis 09nyd8 homo sapien 09bzj1 homo sapien 027199 tetrahymena 09cqc1 mus musculu 09hf03 cryptococcu 091k31 arabidopsis 08x003 neurospora 09y788 neurospora 08y788 neurospora 08wy15 homo sapien 09bzj2 homo sapien 09bzj3 homo sapien 09bzj3 musculu 09t34 mus musculu 09t34 mus musculu	096qd6 homo sapien 012996 homo sapien 014233 schizosacch 041042 plsum satin 014498 homo sapien 09v644 drosophila
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114 125 126 127 127 137 137 137 137 137 137 137 137 137 13	8 6 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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SEQUENCE FROM N.A.
MEDLINE=96127530; PubMed=8590280;
MEDLINE=96127530; PubMed=8590280;
MAGASE T., Seki N., Tanaka A., Ishikawa K., Nomura N.;
"Prediction of the coding sequences of unidentified human genes. IV. The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by analysis of cDNA clones from human cell line KG-1.";
DNA Res. 2:167-174(1995).
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TAOH K., Yang D., Sasatomi T., Nakao M., Shichijo S., Takasu H.,

Matsumoto H., Mori K., Yamana H.;

"SART-3 (Squamous cell carcinoma antigen recognized by T cells).";

Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.

EMBL; D63879; BAA099291; -.

EMBL; AB020880; BAA78384.1; -.
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE 963 AA; 109934 MW; 06B26CEB8B19102A CRC64;
                                                                 Created)
Last sequence update)
Last annotation update)
                                  963 AA.
                                  PRT;
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InterPro; IPR003107; HAT.
InterPro; IPR003504; RNA_rec_mot.
PFdm; PF00076; rrm; 2.
SMART; SM00386; HAT; 6.
SMART; SM00360; RRM; 2.
                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21,
                                  PRELIMINARY;
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Query Match

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                                                                                                                                               Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                           ., Takasu H., Itoh K.; encoding tumor-rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNKNOWN_2.
                                                                       Last annotation update)
                                                                                                                                                                                                                                      STRAIN-BALB/C; TISSUE-SQUAMOUS CELL CARCINOMA;
BELLINE-202349; PUBMed-10761712.
Harada K., Yamada A., Mine T., Rawayoe N., Takasu
"Mouse homologue of the human SART3 gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.7%; Score 4379.5; DB 11
87.0%; Pred. No. 1.6e-254;
iive. 52; Mismatches 70;
                                                        sequence update)
   962
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EMBL, AF172722; AAF55228.1; -.
HSSP, P09012; 201A.
MGD; MG1.1858230; Sart3.
InterPro; IPR003107; HAT.
InterPro; IPR005504; RNA_rec_mot.
                                     Created)
                                                        Last
09JLI8
09JLI8:
01-OCT-2000 (TrEMBLrel. 15, Creat
01-OCT-2000 (TrEMBLrel. 15, Last
01-JUN-2002 (TrEMBLrel. 21, Last
Tumor-rejection antigen SARF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM_RNP_1; UNI
SEQUENCE 962 AA; 109618 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 87.0 Matches 839; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00076; rrm; 2.
SMART; SM00386; HAT; 6.
SMART; SM00360; RRM; 2.
                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=10090;
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Oy 241 AARLEKVHSLFRROLAIPLYDMEATFAEYEEWSEDPIPESVIQNYNKALQOLEKYKPYEE 300		Ecker J.R.; "Arabidopsis cDNA clones."; "Arabidopsis cDNA clones."; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databas EMBL, AY075670; AAL77677.1; SEQUENCE 816 AA; 92808 MW; 2260EDC78469DBAF CRC6/ SEQUENCE 816 AA; 92808 MW; 2260EDC78469DBAF CRC6/ SEQUENCE 816 AA; 92808 MW; 2260EDC78469DBAF CRC6/ Best Local Similarity 28.3%; Pred. No. 6.58-76; Inc. Best Local Similarity 28.3%; Pred. No. 6.58-76; Inc. Best Local Similarity 28.3%; Pred. No. 6.58-76; Inc. Best Local Similarity 18.3%; Pred. No. 6.58-76; Inc. Best Local Similarity 28.3%; Pred. No. 6.58-76. 18.1%; I 1 1 1 1 1 1 1 1 1
Db 541 DYPEHVCEVLLTMERTEGTLEDMDLAIQKTETRLARVNEGRMKAAEKEAALVQQEEEKAE 600 QY 600 QRKRARAEKKKKKIRGPEKGADEDDEKEMGDDEEEQPSKRRRVENSIPAAGETON 659 [11: 11 11 11 11 11 11 11 11 11 11 11 11 11		PRESULT 3 PRELIMINARY; PRT; 364 AA.

	344 PDLWIRYSQYLDRQLKVKDLVLSVHNRAIRNCPWTVALWSRYLLAMERHGVDELDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD	Qy 583 AAEKEAALVQQEEERAAEQRKRARAEKKKKKIRGPEKRGADEDDEKEWGDDEEBQPS 642 1 1 : : : : : :	QY 818 EEICKAHGTVKDLRLVTNRAGKPKGLAYVEYENESQASQAVMKMDGMTIKENIIKVAISN 877 :: : : :	095TW7, 01-MAY-2000 (TERBELFEI. 13, Created) 01-MAY-2000 (TERBELFEI. 13, Last sequence 01-UNY-2002 (TERBELFEI. 21, Last annotatii Hypothetical 87.2 kba protein. 12265-100 OR AT4G24270. Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta; Espermatophyta; Magnoliophyta; eudicotyled eurosids II; Brassicales; Brassicaceae; A
. 491 471 530 609 578 677	PLKEKVYRDECTAFISHLSVKAGEED CYEFKEEKSALQALEMDRKSVEGREWEED AYADFVDDEHLAAAIAKNRKMFGKKISIA PFSCTKEELEEICKAHGTVKDLRLVTNRAGKPI	SULT 5 A30 Q17430 PRELIMINARY; PRT; 836 AA. Q17430; 01-7AN-1999 (TrEMBLrel. 09, Created) 01-7AN-1999 (TrEMBLrel. 21, Last annotation update) 01-JON-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 95.5 kba protein B0035.12 in chromosome IV. B0035.12. Caenorhabditis elegans. Eukaryota: Metazoa; Nemacoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.		Duery Match 17.3%; Score 864; DB 5; 9est Local Similarity 27.7%; Pred. No. 1.36-43; 4atches 256; Conservative 185; Mismatches 366; 65 SDGDEYAMASSAESSPGEYEWEYDEEEEKNQLEIERLEE

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30;
                                                        670
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                                                                                                                                                                                                                                                                                                                                       849
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                                                     GPEKRGADEDDEKEWGDDEEEQPSKR--RRVENSIPAAGE-----TONVEVAAGPAGKC
                                                                                   142 FPLTEELWLEWLHDEISMAQDGLDREHVYDLFEKAVKDYICPNIWLEYGQYSVGGIGQKG
                                                                                                                                                AAVDVEPPSKQKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSMQEPDTKLRPLFEACG
                                                                                                                                                                                                                                             EVVQIRPI-FSNRGDFRGYCYVEFKEEKSALQALEMDRKSVEGRPMFVSPCVDKSKNPDF
                                                                                                                                                                                                                                                                                                                                     790 KVFRYSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTNRAGKPKGLAYVEYE
                                                                                                                                                                                                                                                                                                                                                                                   -----KKGK-----KEFTRRGNDGSGNSKDPSLISEKAKAPLG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1014 AA; 118008 MW; 45E15A7435EB08CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oliver K., Harris D., Lyne M.H., Rajandream M.A., Barrel Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AL109934; CAB5740.1; -.. InterPro; IPR003107; HAT. InterPro; IPR003504; RNA_rec_mot. PF00076; rrm; 4. SMART; SM00366; HAT; 2. SWART; SM00366; RRM; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            090SY2;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to C-term of yeast U4/U6 splicing factor PRP24.
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PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1
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       492 LEHFDLAVOKVMPRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEKAVKDYICPNIWLEYGQY----SVGGIGQKGGLEKVRSVFERALSSVGLHMTKGLA 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331. LIFERALVENCLVPDLWIRYSQYLDRQLKVKDLVLSVHNRAIRNCPWTVALWSRYLLAME 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 RALEYLKQEVEERFNESGDPSCVIMQN------WARIEARLCNNMQKARELWDSIM 500
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                                                                                                                                                                                                                                                                                 Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P.,
Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                           Bancroft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 768;
                                                                  Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Banc
Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                          SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; ALOY8637; CAB45662.1;
EMBL; AL161561; CAB79337.1;
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Best Local Similarity 27.7%; Pred. No. 3.3e-41;
Matches 264; Conservative 140; Mismatches 306;
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PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003107; HAT.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 768 AA; 87171 MW;
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SMART; SM00386; HAT; 3.
SMART; SM00360; RRM; 1.
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                                            SEQUENCE FROM N.A.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                            471 STMKYNPELA---AETLKKSLYKNV----DQPQ-----LLFQFYQSIMDLNNDCFTNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: | | :: | | : | CKDVKVAQIEFSETSEVLAAKTRDLKSIRGHEISVQIHVDTNLYVTNFPPTYDELD--IT
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                                                                                                                         DLWIRYSQYLDRQLKVKDLVLSVHNRAIRNCPWTVALWSRYLLAMERHGVDHQVISVTFE
                                                                                                                                                          ELWLQYTAWLSKVDFSSSQASSVAERATRNCSWIGRIWSIKLTYMTLSGASTSAVCEEKD
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                                                                                                                                                                                                                                                                                                    NHKGSKD-----ARMRIELSKIYLYSEISDFESVEKCW-SDMFHDFQNQALYWISRYI
                                                                                                                                                                                                                                                                                                                                          ---YYNLERAHGDTQHCRKALHRAVQCTSDYPEHVCEVLLTMERTEGSLEDWDIAVQKTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDEKEWGD-DEEEQPSKRRR-----VENSIPAAGETQNVEVAAGPAGKCAAVDVEPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  781 VDKSKNPDFKVFRYSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTNRAGKP
                                                                                                                                                                                              KALNAGFIQATDYVEIWQAYLDYLRRRVDFKQDSSKELEELRAAFTRALEYLKQEVEERF
                                                                                                                                                                                                                                                                   NESGDPSCVIMQNWARIEARL------CUNMQKARELWDSIMTRGNAKYANMWLE---
                                                                                                                                                                                                                                                                                                                                                                                                             571 TRLARVNEQRM----KAAEKEAALVQQEEEKAEQRKRARAEKKALKKKKKIRGPEKRGADE
                                                                                                                                                                                                                                                                                                                                                                                                                                              HLYDVLNAQRISFKRQLDSFAEETKQTVENTEPLKVPQADDTAALSKKRKPGQE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BERKELEY;
MEDLINE=20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Blarandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         841 KGLAYVEYENESQASQAVMKMDGMTIKENIIKVAISNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         796 KGFGYVVMTTNQDAENA-LSAAGKQLGNRVLNVVLSKP
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09W4D2;
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RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botcher P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Barris N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heinan T.J., Wein M. H., Ibegwam C.,
RA Harris N.L., Harvey D., Heinan T.J., Wein M. H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Wei M. H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Wei M. H., Ibegwam C.,
RA Martei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mertulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pacleb J.M.,
RA Reinert X., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Syler E., Spradling A.C., Stapleton M., Strupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Strupski M., Wang S., Yao Q. A.,
Williams S.M., Woodage T., Worlay M., Wang S., Yao Q. A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho Q., Zheng L.,
Rhe genome sequence of Drosophila melanogaster.",
Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 LEYGQYSVGGIGQKGGLEKVRSVFERALSSVGLHMTKGLALWEAYREFESAIVEAARLEK
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Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (COT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR603433; AAF46021.
EMBL, AV61395; AAL28943.1; -.
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PROSITE; PS00030; RRM_RNP_1; 1.
SEQUENCE 941 AA; 106739 MW; EAF2775B499FECFD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 IPLSEYVVNYLVDQGNVQN------
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FlyBase; FBGN0014024; Rnp4F.
InterPro; IPR003107; HAT.
InterPro; IPR000564; RNA_rec_mot.
Pfam; PF00076; rrm; I.
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SMART; SM00360; RRM; 1.
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OC Ephydroidea; Drosophilidae; Drosophila. NCBL_TaxID=7227; RN (1) RS SEQUENCE FROM N.A. TISSUEBADULT HEAD; RA PETSCHE*ADULT HEAD; RA Genee 0:0-0(0). RA Genee 0:0-0(0). RA GRA7551; CAA75535.1: -		SEGUENCE 943 AA; 10700 MW; 4623DECB27059416 CRC64;	Query Match 8.4%; Score 420; DB 5; Length 943; Best Local Similarity 20.2%; Pred. No. 6.7e-17; Matches 220; Conservative 152; Mismatches 349; Indels 370; Gaps	Qy 7 TSASEPEAESKAGPKADGEEDEVKAARTRRKVLSRAVAAATYKTWGPAWDQQEEGVSESD 66	QY 67 GDEYAMASSAESSPGEYEWEYDEEEEKNQLEIERLEEQLSINVYDYNCHVDLIRLERLEG 126	QY 127 ELTKVRMARQKMSEIFPLTEELWLEWLHDEISMAQDGLDREHVYDLFEKAVKDYICPNIW 186	QY 187 LEYGQYSVGGIGQKGGLEKVRSVFERALSSVGLHMTKGLALWEAYREFESAIVEAARLEK 246 :	OY 247 VHSLFRRQLAIPLYDMEATFAEYEEWSEDFIPESVIONYNKA 288 ::	ALLQAEAPRLAEYQAYI-DFE-MKIGDPARIOLIFERALVENCLV ::: : : : : :	QY 344 PDLWIRYSQYLDRQLKVKDLVLSVHNRAIRNCP 376	QY 377 WTVALWSRYLLAMERHGVDHQVISVTFEKALNAGFIQATDYVEIWQAYLDYLRRRV-D 433 :	QY 434 FKQDSSKELEELRAAFTRALEYLKQEVEERFNESGDPSCVIMQNWARIEARLCNNWQKAR 493 ::	QY 494 ELWDSIM-TRGNAKYANWMLEYYNLERAHGDTQHCRKALHRAVQCTSDYPEHVCEV 548	QY 549 LLTMERTEGSLEDWDIAVQKTETRLARVNEQRMKAAEKEAALVQQEEEKAEQRK 602	Qy 603 RARAEKKALKKKKIRGPEKRGADEDDEKEMGDDEEEQPSKRRRVENSIPAAGETQNVEV 662 1	663 AAGPAGKCAAVDVEPPSKQKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSMQEPDTKL
VHSLFRQLAIPLYDMEATFAEYEE	33.2.6	493 542	OCTSDYPEHVCEV 548 :	602	ronvev 662	SPDTKL 722	RPLFEACGEVVQIRPIFSNRGDFRGYVBFKEEKSALQALEMDRKSVBGRPMFVSPCVD 782 D) D) D) D) D) D)	EICKAHGTWKDLRIVTNRAGKPKG 842 	PMLLPQ 901	TYGARGKGRTQLSLLPRALQRPSAAAPQAENGPAAPAVAAPAAT 946	M 951	GDVQRADEQRGEEQRGEEPRGEEPRGEEQRGUDQLGEEQSGVEQRGDERREEEMPAAVPK 929 SNADFAKLFLR 962 CANADEARTET 962 DD	· ·			Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
247 VHSLFRRQLAIPLYDMEATFAEYEE 1	344 PDLWIRYSOYLD		494 ELWDSIM-TRGNAKYANMWLEYYNLERAHGDTQHCRKALHRAV 	549 LLTMERTEGSLEDWDIAVQ 600 FRRYERCYGTYESIAACQALDLPVE	603 RARAEKKALKKKKIRGPERRGADE 	663 AAGPAGKCAAVDVEPPSKQKEKAAS			843 LAYVEYENESQASQAVMKMDGMTIK	902 TYGARGKGRTQLSLLPRALQRPSAA 			SNDDF RRLF LA	PRELIMINARY; PRT; 2; 2; Create (TrEMBLrel. 05, Create	N-1998 (TrEMBLrel. 05, Last s N-2002 (TrEMBLrel. 21, Last a Inding protein. OR 4F-RNP OR CG3312	phila melanogaster (Fruit fly yota; Metazoa; Arthropoda; Tr gota; Neoptera; Endopterygota

595 EEKAEQRKRARAEKKALKKKKIRGPEKRGADEDDEKEWGD 220 EHIRAYESQALEASAAAAAQALGKOQDODDANAGVKRKWEAIASGETPESATKKP	OY 636	Qy 716 QEPDTKLRPLFBACGEVVQIRPIFSNRGDFRGYCYVEFKEEKSALQALEMDRKSVEGRPM 775 Db 1 1 1 1 1 1 1 1 1 1	Qy 836 RAGKPKGLAYVEYENESQASQAVWKMDGMTIKENIIKVAISNPPQRKVPEKPETR 890 11: : 1: : : : : : : : :	OY 909	RESULT 11 Q06459 ID Q06459 DT Q100459; PRELIMINARY; PRT; 705 AA. AC Q06459; DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) DT 01-NOV-1996 (TrEMBLrel. 21, Last annotation update) DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DE Nucleolin. S Xenopus laevis (African clawed frog). C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; C Amphibia; Batrachia; Annra; Mesobatrachia; Pipoidea; Pipidae; C Xenopodinae; Xenopus.		SEQUENCE Duery Match Best Local (Matches 10:
CVD	783 KSKNPDFKVFRYSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTNRAGK 783 KSKNPDFKVFRYSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTNRAGK 717FRYSPNMEINKIFVRNLHPACSKBELHELFSPFGTIKDVRLVHKLNKQ 843 LAYVEYENESQASQAVMKMDGMTIKENIIKVAISNPPORKVPE-KPETTKRAPGGPML	Db 768 IAYVEFEKPGEAQRAVAGRDGCLFKGMNISVAISNPPPRGTSAVKPSVAP 817 Qy 902 TYGARGKGRTQLSLLPRALQRPSAAAPQAENGPAAAPAAT 946 Db 818KRRVPTSLIPTTLVRQEVAAKKLRLLLPEPGDISSTSASVDVAIKREANGEEQK 871 Qy 947	Db 872 GDVQERDEQKGEEQKGEEQKGEEKGDDQIGEEQSGVEQKGDEKKEEEMPAAVPK 931 QY 952 SNADFAKLFLR 962 Db 932 SNDDFRKLFLK 942 RESULT 10	001491 D 001491 AC 01491; AC 01491; DT 01-NOV-1996 (TrEMBLrel. 01, Created) DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DE Colony 1. GN COLI. OS Ophiostoma ulmi (Dutch elm disease fungus). OC Elkaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; OC Ophiostomatales; Ophiostomataceae; Ophiostoma.	RP SEQUENCE FROM N.A. RC STRAIN-MH75; RA ROYET J.C., Hintz W.E., Bowden C., Kokurewicz K., Li A., Hubbes M.; RL Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases. BR Interpro; IPR000504; RNA_rec_mot. BR Ffam; PF00076; rrm; 4. BR SWART; SM00360; RRW; 4. BR PROSITE; PS50102; RRW; 4. BR PROSITE; PS501023; RRW; 4. BR PROSITE; PS00030; RRW; 9C19CCB96B67EF46 CRC64; Query Watch 7.0%; Score 349; DB 3: Length 826:	Similarity 22.0%; Pred. No. 1 = 12; B: Conservative 100; Mismatches 266; MERHGVDHQVISVTFEKALNAGFIQATDYVEIWOAYLDY	QY 538 TS-DYPEHVCEVLLTMERTEGSLEDWDIAVQKTETRLARVNEQRMKAAEKEAALVQQE 594 165 SQLNWPERVIEIXVKHCNDFESSDVLQNALDEVHNLQRVIAQRRKDATAAQTAQA 219

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30;
                                                                                                                                                                                                   SYDEEEEKNQLEIERLEEQLSINVYDYNCHVDLIRLLRLE-------GELT 129
                                                                                                                                                                                                                            MARQKMSEIFPLTEELWLEWLHDEISMAQDGLDREHVYDLFEKAVKDYICP---NIW 186
                                                                                                                                                                                                                                                                                                               ------KQDSSK-----ELEELRAAFTRALEYLKQEVEERFNESGDPSCVIM 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WARIEARL-----CUNMOKARELWDSIM 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLEKVHSLFRRQLAIPLYDME--ATFAEYEE------WSEDPIPE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----FERALVENCLVPDLWIRYSQYLDRQLKVKDLVLSVHNRAIRNCP--WTVAL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XYLLAMERHGVDHQVISVTFEKALNAGFIQATD-----YVEIWQAYLDYLRRRVD 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAKYANMWLEYYNLERAHGDTQHCRKALHRAVQCTSDYPEH----VCEVLLTMERTE 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SY------MEEVIENIPGARQIFER-----WIEWEPPEQAMQTYINFELRYK 201
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                                                                                                                                                gvkaartrrkvlsravaaatyktmgpawdQ--Qeegvsesdgdeyamassaesspgey 83
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
                                                                                Gaps
                                    5.6%; Score 280; DB 5; Length 744;
.larity 20.1%; Pred. No. 1.2e-08;
Conservative 130; Mismatches 272; Indels 208;
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44 AA; 87984 MW; 523A82E5F1678C29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEDWDIAVQKTETRLARVNEQRMKAAEKEAALVQQEE----
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Last sequence update)
Last annotation update)
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(TrEMBLrel. 15, I
(TrEMBLrel. 21, I
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27;
----DDYIE 556
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                                                                                                                                                                                                                                                                                                                                                                          397 QVISVTFEKALNAGFIQATDYVEIWQAYLDYLRRRVDFKQDSSKELEELRAAFTRAL--- 453
                                                                                                                                                                                                                                                                                                                                                                                                                             747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EYLKQEVE------ERFNESGDPSCVIMQNWARIEARLCNNMQKAREL 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEGSLE-----DWDIAVQKTETRLARVNEQRMKAAEKEAALVQQE------EEKAE 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           862 FEMGLSHGDSGPDAELNVQLARRIYERANEMLRQLGDKESRVLLLEAWRDFERDASDSQE 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRKRARAEKKALKKKKI---RCPEKRGADEDDEKEWGDDEEEQPSK-----RRRV 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     922 MQKVMDKMPRRIKKRQKIVSDNGVEE-GWEEVFDYIFPEDEMARPNLKLLAAAKMWKTQK 980
                                                                                                                                                                                            ----IAFARFEEGOKEHDRARIIYKY--ALDHLP
                                                                                                                                                                                                                                                                                                                                                                                                                             ERTROIYKTCLELIPHKOFTFSKLWLLYAOFEIR------CKELORARKALGLAIGMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496 WDSIMTRGNAKYAN-MWLEYYNLERAHGDTQHCRKALHRAVQCTSDYPEHVCEVLLTMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Cell cycle control crn (crooked neck) protein-like.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsyta; Viridiplantae; Streptophyta; Eukaryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudiocytledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                     FESAIVEAARLEKVHSLFRRQLAIPLYDMEATFAEYEEWSEDPIPESVIONYNKALQQLE
                                                                                                                                                             KYKPYEEALLQAEAPRLAEYQAYIDFEMKIGDPARIQLI - - - - - FERALVENCLVPD
                                                                                                                                                                                                                                                                  346 LWIRYSQYLDRQLKVKDLVLSVHNRAIRNCP-----WT--VALWSRYLLAMERHGVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-COLUMBIA;
MEDLINE-99087483; PubMed-9872454;
Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
Sequence features of the regions of 1,013,767 bp covered by sixteen
physically assigned P1 and TAC clones.";
DNA Res. 5:297-308(1998).
EMBL, AB016871; BAB10652.1; -.
InterPro; IPR0013107; HAT.
InterPro; IPR001440; TPR.
Ffam; PF02184; HAT. 11.
SMART; SM00386; HAT, 13.
SEQUENCE 665 AA; 80016 MW; IDB652B537D87391 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.3%; Score 263.5; DB 10; Length 665; 19.1%; Pred. No. 1e-07;
513 FV--YVHPDVKNWIKFARFE----ESHGFIHGSRRVFERAVEFFG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENSI---PAAGETQNVEVAAGPAGKCAAVDVEPPSKQKE 683
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Matches 130; Conservative 132; Mismatches 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                          294
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Bankins R.A., Galle R.E.,
R. Sutton G.C., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.C., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Piefifer B.D.,
RA Mank M., Doyle C., Baxter E.G., Helt G., Change M., Miklos G.L.G.,
RA Ballew R.M., Basun A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Benns P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burkus K.C., Bucchan M.R., Bouck J., Broketein P., Brothar I.,
RA Burkus K.C., Bucam D.A., Buller H., Cadlew E., Center A., Chandra I.,
RA Burkus K.C., Bucam D.A., Buller H., Cadlew E., Center A., Chandra I.,
RA Burkus K.C., Buchan M.R., Bouck J., Broketein P., Brothar I.,
RA Cadley S., Dahlke C., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Burkus K.C., Gabrielisa C.C., Ferraz C., Ferriard S., Felsschman W.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
Jolall M., Kaluh F., Karpen G.H., Ke. Z., Kennison J.A., Ketchhun K.A.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
Jolall M., Kaluh F., Karpen G.H., Ke. Z., Kennison J.A., Ketchhun K.A.,
Alasko P., Leil Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Alasko P., Leil Y., Levitsky A.A., Li J., Li Z., Liang Y., Moshrefi A.,
Rander S.M., Moy M., Murphy B., Worther D., Worlerson D.,
Rander K., Meyer M., Murphy B., Worler E., Wang A.,
Reinert K., Remington K.A., Mixon K., Wusskern D.R., Pacieb J.M.,
Rander E., Siden-Klamos I., Simpson M., Strong R., Such K., Shen H.,
Rander E., Wassarman D.A., Weinstcok G., Wang S., Zhao Q., Zhao Q., Zhao G., Stander S., Wulliams S.M., Woodage T., Worley K.C., Wu D., Yung G., Zhao Q., Zhao R., Williams S.M., Woodage T., Worley R., Stone S., Scheeler F., Shen F., Scheeler F., Rander S., Pollard J., Shang S., Bulls R., Scheeler F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E--YDEEEEKNQL-----EIERLEEQLS------INVYDYNCHVDLIRLLR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 LEGELTKVRMARQKMSEIFPLTEELWLEWLHDE-----ISMAQDGLDREHVYDLFEK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 AVKDYICPNI--WLEYGOYSVGGIGOKGGLEKVRSVFERALSSVGLHMTKGLALWEAYRE 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDEVKAARTRRKVLSRAVAAATYKTMGPAWDQQEEGVSESDGDEYAMASSAESSPGEYEW
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InterPro: IPR001201; CRL_TRIO.
InterPro: IPR001071; RefBind/tocTrans.
InterPro: IPR001071; RefBind/tocTrans.
InterPro: IPR001440; TPR
InterPro: IPR00184; HAT; 10.
InterPro: IPR0188; CRL_TRIO; 1.
InterPro: IPR00188; HAT; 10.
IPRINTS; PR00188; HAT; 10.
IPRINTS; PR00188; HAT; 11.
IPROFILE 1305 AA; 153207 WW; 1C8D5BE5EEID49DA CRC64;
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MEDLINE-99419025; PubMed=10488083;
Sorokina E.A., Kleinman J.G.;
"Cloning and preliminary characterization of a calcium-binding proteir closely related to nucleolin on the apical surface of inner medullary collecting duct cells.";
J. Biol. Chem. 274:27491-27496(1999).
HSSP; P09651; 1HA1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                          EARERQEAEIRPPKOKITDSTELSDY-----RLRRRKEFEDQIRRARWNI---
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iive 71; Mismatches 141;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

Tumour antigen protein; SART-3; cytotoxic T-cell; HLA antigen; Tumour antigen protein SART-3 encoding DNA (SUMU) SUMITOMO PHARM CO LTD. (ITOH/) ITOH K. AAZ90783 standard; DNA; 3798 99WO-JP04622 98JP-0242660 23-JUN-2000 (first entry) WPI; 2000-237868/20. P-PSDB; AAY85422. toh K, Nakao M; WO200012701-A1 Homo sapiens 27-AUG-1999; 28-AUG-1998; 09-MAR-2000. tumour; ds AAZ90783; RESULT 1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

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Tumor antigen protein SART-3 recognized by cytotoxic T-cells binding

Human testicular a DNA encoding novel Human secreted exp

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Human Human Human

Tumour antigen pro Human SART3-IC-HER

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Length

Query Match

Score 3798 2886

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                    This DNA encodes a tumour antigen protein (SART-3) which is recognized by cytotoxic T-cells binding to HLA antigen. SART-3 can be expressed by standard recombinant methodology. SART-3 and its peptide derivatives can be used in the prevention, treatment and diagnosis of tumours in vitro or in vivo.
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1911 AMANAGACHACCHANGCCHANGGCCCGAAANCHCCTGCCGCTGCGCTGCAGCTGCACTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTGCACCTCCCTC	Oy 3061 GTCAAGAGCCTTTCAGTGCTCCTCATATTGAGGGCAGTGGCAGAAAAGTGACCACTCTG 3120 Db 3061 GTCAAGAGCCTTTCAGTGCTCCCTCATATTGAGGGCAGAAAAGTGACACTCTG 3120 Qy 3121 CAGGCTGGGCCCAGGATGTGGTGTCCTGAGATAGTTTGTATCTTAAAGACTGAGGCACA 3180 Db 3121 CAGGCTGGGCCCAGGATGTGGTGTCCTGAGATAGTTTTTTTT	3181 GAAGCGAAACGACACTGTTTTTGAGACACATTGTCCAAATGTTTTTGGCCAGCT	OY 3241 CGGCCCCTTTGIACACACTTCACCCGCACACAGGGCCCGCGGTTTC 3300 3241 CGGCCCCTTTTGIALIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 3361 GGTGGGTCTGAGGGAAGTCAGCTATAAAACATTTGCTGGAGTTTTGTTCAATGGGGCTGT 3420		3541 TITICITIGCCTAGTGACTAGTGACTGTGTTGTTGTAAACATGAGTTTCAGCCCTTTGGT	3601 TTGTTRATACCAGGCAAAGGAAACTTCAATTCTCCCCATTTAGGTTTATTAACTG 111111111111111111111111111111111111	3661 ACGTTCTCTTCAAACTTCTTGCTCAATGCTACTCAGATGTCCATTCACATACAGATGTC	3721 3721	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	RESULT 2 AAD21574 ID AAD21574 standard; DNA; 3537 BP.	AX AAD21574; XX XX DT 28-JAN-2002 (first entry)		<pre>KW inmunostinunatory component; T-cell mediated inmune response; UC; KW dendritic cell; colon cancer; breast carcinoma; ovarian cancer; KW human; HER-2 membrane distal intracellular domain; SART3-IC; KW squamous cell carcinoma antigen; fusion DNA; ds.</pre>	AA OS Homo sapiens. XX XX FH Key Location/Qualifiers
	1921 AAGAAGAGCAGCTTCCAAACGCAGAAGGGTCGAGAACAGCATCCCTGCAGCTGGAGAAA 1981 CACAAAATGTAGAAGTAGCAGGGCCCGCTGGGAAATGTGCTGCCGTAGATGTGGAGC 111111111111111111111111111111111	2041 CCCCTTCGAAGGAGAAGGCAGCACCTCCCTGAAGGGGACATGCCCAAGGTGCTGC 2101 ACGACAGCAGCAAGGACAGCATCACCGTCTTTGTCAGCAACCTGCCCTACAGGATGCAGG 1111111111111111111111111111111111	2161 AGCCGGACACGAACCTCAGGCCACTCTTCAAGGCCTGTGGGAAGGTGGTCCAGATCCGAC	221 CCATCTTCAGCAACCGTGGGGATTTCCGAGGTTACTGCTACGTGGAGTTTAAAGAGGGA 2281 AATCAGCCCTTCAGGCACTGGAGATGGACCGGAAAAGTGTAGAAGGGAGGCCAATGTTTG	241 TTCCCCCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TAGAAGAAATCTGTAAGGCTCATGGCACCGTGAAGGACCTCAGGCTGGTCACCAACCGGG	CTGGCAAACCAAAGGCCTGGCCTACGTGGAGTATGAAAATGAATCCCAGGCGTCGCAGG 	CTGTGATGAAGATGGACGCATGACTATCAAAGAGAACATCATCAAAGTGGCAATCAGCA 	ACCTCCTCAGAGGAAAGTTCCAGAGAAGCCAGAGACCAGGAAGGCACCAGGTGGCCCCA	TGCTTTTGCCGCAGACATACGGAGCGAGGGGAAGGGAAG	CTCGTGCCCTGCAGCGCCCAAGTGCTGCAGCTCCTCAGGCTGAGAACGGCCCTGCCGCGGGCTLIIIIIIIIIIIIIIIIIIIIII	2821 CTCCTGCAGTTGCCGCCCAGCACCACGAGGCACCCAAGATGTCCAATGCCGATTTTG	2881 CCAAGCTGTTTCTGAGAAAGTGAACGGGACGCTGGGAGACAGGAAATGCCTTACTTCACT	2941 CTGGCCCGGCGGACCTCCCACCACCCAGCAGTGCACTGGGGATGGACAGCCTGGTGTCCACTGCTGTGCTGTGTGCTGTGTGTG	TGCGTGCTCGCAACCAGATGGCTCCTCGGCTTTAGACAGAAAGGGGAAGGGGTTCTAA

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/*tag= a
/product= "Human SART3-IC-mature HER-2 membr
distal intracellular domain fusion protein"
/note= "CDS does not include stop codon"
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16; Conservative 0; Mismatches
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or research purposes. The prostate cancer antigens may be used to treadisorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infections diseases. AAR16506 to AAR16514 to AAB57303 represent sequences used in the exemplification of the presen
                                                                                                                                                               AATITCTGTAACCTTCGAGAAGCTTTGAATGCCGGCTTCATCCAGGCCACTGATTATGT
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	CC The invention relates to nucleic acids (AA198058-AA198161) or their cC homologues expressed by human neuroblastoms useful for detecting genes CC expressed by neuroblastomm and for analysing their structure and CC inction. The nucleic acids are useful for the diagnosis and prognosis of	Sequence	Query Match 35.1%; Score 1331.2; DB 22; Length 1403; Best Local Similarity 99.8%; Pred. No. 0; Matches 1333; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	QY 2340 GTTTCCCCTGTGTGGATAAGAGCAAAACCCCGATTTAAGGTGTTCAGGTACTAGCACT 2399	OY 2400 TCCCTAGAGAAACACAGCTGTTCATCTCAGGCCTGCCTTTCTCTGTACTAAGAGGAA 2459 111111111111111111111111111111111111	QY 2460 CTAGAAGAAATCTGTAAGGCTCATGGCACCTGAAGGACCTCAGGCTGGTCACCAACGGG 2519	OY 2520 GCTGGCAAACCAAAGGCCTGGCCTACGTGCAGTATGAAAATGAATCCCAGGCGTCGCAG 2579	OY 2580 GCTGTGATGAGGACGCCATGACTATCAAAGAGAACATCATCAAAGTGGCAATCAGC 2639	QY 2640 AACCTCCTCAGAGGAAAGTTCCAGAGAAGCCAGGAAGGCACCAGGTGGCCCC 2699 	QY 2700 ATGCTTTTGCCGCAGACGTACGGAGCGGAAGGGAAGGGA	Qy 2760 CCTCGTGCCCTGCAGGCCCCAAGTGCTGCAGGCTCAGGCTGAGAACGGCCCTGCCGCG 2819 Db 429 CCTCGTGCAGCGCCCAAGTGCTGCAGCTCCTCAGGCTGAGAACGCCCTGCCGCG 488	QY 2820 GCTCCTGCAGTTGCCGCCCCAGCAGCCACCCAAGATGTCCAATGCCGATTTT 2879	QY 2880 GCCAAGCTGTTCTGAGAAAGTGAACGGGACGCTGGGAACAGGAAATGCCTTACTTCAC 2939 	QY 2940 TCTGGCCGGGGACCTCCCACCACCCAGGGGACTGGACAGGCCTGGTGTG 2999	Qy 3000 CTGCGTGCTCGCAACCACAGATGGCTCCTCGGCTTTAGACAGAAAGGGGAAGGGGTTCTA 3059	QY 3060 AGTCAAGAGCCTTTCAGTGCTCCCTCATATTGAGGCAGTGGCAGAAAAGTGACCACTCT 3119	Oy 3120 GCAGGCTGGGCCCAGGATGTGGTGTCCTGAGATAGTTTTGTATCTTAAAGACTGAGGCAC 3179	QY 3180 AGAAGCGAAACGAGAACACATGTTTTGAGACACAGTTGTCCAAATGTTTCTGGCCAGC 3239
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2000US-0246474.
2000US-0246475.
2000US-0246476.
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                                              CTTTTAATTTTAAAAGATGAAATGGCAGATGCTAGTAATTCACAGAATGGCCTCTTGTGG
                                                                         GGGTGGGTCTGAGGGAAGTCAGCTATAAAACATTTGCTGGAGTTTTGTTCAATGGGGCTG
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 TGCAGCTCCTCAGGCTGAGAACGGCCCTGCCGCGGCTCCTGCAGTTGCCGCCCCAGCAGC
                                              2846 CACCGAGGCACCCAAGATGTCCAATGCCGATTTTGCCAAGCTGTTTCTGAGAAAGTGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding a reproductive system antigen or ameliorating a medical condition
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Pred. No. 1.5e-275;
0; Mismatches 1;
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2000US-0246610.
2000US-0246611.
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2000US-0250391
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Best Local Similarity 99.9%;
Matches 1057; Conservative
                                                                               2000US-0246528
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2000US-0249207
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                                       Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ds.
                           Human testicular antigen encoding DNA fragment SEQ ID NO: 2196.
                                                                                                                  17-JAN-2001; 2001WO-US01329
             (first entry)
                                                                                       WO200155317-A2
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14-SEP-2000,
             21-JUN-2002
                                                                          Homo sapiens
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                                                                                                          3386 AAAACATTTGCTGGAGTTTTGTTCAATGGGGCTGTGCATTTTTATATATGTGTGTTTGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel human diagnostic protein #26940.
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2000US-0649167
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                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of 973 mean testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and sastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTCCACCCTGCACAGCACATGTGCCCGTCATTTTAATTTTAAAAGATGAAATGC
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                                                                                                                                                                                                                                    Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer
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2000US-0256719.
2000US-0251479.
2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251989.
                                                                                                                                                HUMAN GENOME SCI INC
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                                                                                                      2000US-0254097
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Matches 1057; Conservative
                                                                                                                                                                             Rosen CA, Barash SC,
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                            08-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
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Cor identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in clayoratics, forensics, gene mapping, identification of mutations responsible for genefic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human or degenerate data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO. It fip. wipo.int,pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1946 AAGGGTCGAGAACAGCATCCCTGCAGCTGGAGAAACACAAAATGTAGAAGTAGCAGCAGG 2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCCGCTGGGAAATGTGCCGTAGATGTGGAGCCCCCTTCGAAGCAGAAGGAAAGGC
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1344 BP; 348 A; 311 C; 365 G; 320 T; 0 other;
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100.0%; Pred. No. ...
0; Mismatches
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tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from numan, mouse, chicken and rat tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include: Chemotactic; proliferative; immunomodulatory; haematopoietic; chemotactic; antibacterial; antifungal; antiviral; antibabeterial; antifungal; antiviral; antidiabetic; antipartimatic; vulnerary; antiulcer; osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The SESTs can be used for gene therapy and in vaccines. The SESTs can be used for gene therapy and in vaccines. The SESTs are useful as probes for the molecules which correspond to the SESTs. Proteins encoded by the SESTs are useful in assays for determining biological activity and raising are useful in assays for determining biological activity and raising are useful in assays for determining biological activity and raising (multipole scherosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatorry disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45926 to AAA45931 represent linker variants which are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 AACGTCTATGACTACAACTGCCATGTGGACTTGATCAGACTGCTCAGGCTGGAAGGGGAG 392
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immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA43426 to AAA45925 represent specifically claimed secreted expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 GACGAAGAGGAGGAGAAAAACCAGCTGGAGATTGAGAGACTGGAGGAGCAGTTGTCTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; tumour; infection; depression; psoriasis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 437 BP; 113 A; 87 C; 133 G; 104 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the exemplification of the present invention.
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99.0%; Pred. No. 1.16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 343; 803pp; English.
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Matches 411; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McCoy JM,
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                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (III) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II).

COPULATION OF (III) and tigen presenting cells that express (III).

COPULATION OF (III) and tigen presenting cells that express (III).

COPULATION OF (III) and cativity. An oligonucleotide (IV) that hybridises to (IV) has cytostatic activity. An oligonucleotide (IV) that hybridises to (SI) can be used for detecting ovarian cancer in a patient of polynucleotide hybridising to (IV) and comparing the amount of polynucleotide hybridising to (IV) and comparing the amount to patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polynucleotide hybridising to (IV) is detected preferably by polynucleotide hybridising and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells
                                                          512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a composition (I) comprising: carriers
          CTTACCAAGGTGAGGATGGCCCGCCAGAAGATGAGTGAAATCTTTCCCTTGACTGAAGAG
                    CTCTGGCTGGAGTGGCTGCATGACGAGATCAGCATGGCCCAGGATGGCCTGGACAGAGAG
                                                                       CACGTGTATGACCTCTTTGAGAAAGCCGTGAAGGATTACATTTGTCCTAACATTTGGCTA
                                                                                                                                CACGTGTATGACCTCTTTGAGAAAGCTGTGAAGGATTACATTTGTCCTAACATTTGGCTA
                                                                                                                                                         GAGTATGGCCAGTACTCAGTTGGTGGGATTGGTCAGAAAGGTGGCCTTGAGAAAGTTCGC
                                                                                                                                                                       Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or I cell expressing
                                                                                                                                                                                                            TCCGTGTTTGAAAGGGCTCTCTCGTCTGTTGGTTTACATATGACCAAAGGACTCG
                                                                                                                                                                                                                                                                                                                                                                                                  Human; ovarian cancer; ovarian tumour; cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                                           Human ovarian cancer related cDNA clone SEQ ID NO:1728.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                 61
with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known
                                                                                                                                                                                                                                                                                                                                                                              3422 CATTTTT-ATATTATGTGTTTGTAAATGACATGTCAGCCCTTGTTTCATGTTTCCTAAAA
                                                                                                                                                                                                                              3063 CAAGAGCCTTTCAGTGCTCCCTCATATTGAGGGCAGTGGCAGAAAAGTGACCACTCTGCA
                                                                                                                                                                                                                                                                                                      3123 GGCTGGGCCCAGGATGTGGTGTCCTGAGATAGTTTTGTATCTTAAAGACTGAGGCACAGA
                                                                                                                                                                                                                                                                                                                          181 CGGCCCCTTTTTGTATGACACTTCTTTCCACCCTGCACAGCACATGTGCCCGTCATTCT
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                                                                                                                                                                                                                                                  2 CAAGAGCCTTTCAGTGCTCCCTCATATTGAGGGCAGTGGCAGAAAAGTGACCACTCTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ovarian cancer related cDNA clone SEQ ID NO: 2028.
                                                                                                                 BP; 108 A; 86 C; 105 G; 132 T; 1 other;
                                                                                                                                                  Score 393.4; DB 24;
Pred. No. 2.1e-96;
0; Mismatches 2;
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                                                                                                                                                  10.4%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-2001; 2001WO-US17756
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                                                                                                                                                                         Best Local Similarity 98.8
Matches 427; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 GCAGAATATTTG
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                                                                                                                                                                       Similarity
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                                                                                                                 Sequence 432
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                                                                              techniques
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(first entry)

10-0CT-2001

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and immunostimularits; and a polypeptide (II) of a ovarian tumour polypeptide and immunostimularits; and a polypeptide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II).

(I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells with (III) or (II). (III) is useful in design and preparation of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a rechniques.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09
                                                                                                                        present invention describes a composition (I) comprising: carriers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3064 AAGAGCCTTTCAGTGCTCCCTCATATTGAGGGCAGTGGCAGAAAAGTGACCACTCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGGGCCCAGGATGTGGTGTCCTGAGATAGTTTTGTATCTTAAAGACTGAGGCACAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTT-ATATTATGTGTTTGTAAATGACATGTCAGCCCTTGTTTCATGTTTCCTAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGAAACGAGAACAC - CTGTTTTTGAGACACAGTTGTCCAAATGTTTCTGGCCAGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GCGAAACGAGAACACCTGTTTTTGAGACACAGTTGTCCAAATGTTTCTGGCCAGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAATTTTAAAAGATGAAATGGCAGATGCTAGTAATTCACAGAATGGCCTCTTGTGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGTCTGAGGGAAGTCAGCTATAAAACATTTGCTGGAGTTTTGTTCAATGGGGCTGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or I cell expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 430 BP; 108 A; 85 C; 104 G; 132 T; 1 other;
                                                                                       Claim 1; SEQ ID 2028; 489pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426; Conservative
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                                                   polypeptide
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AAH98082;

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7-transmembrane G-protein coupled protein receptors (7TM-GPCRS). The present sequence is one such murine 7TM-GPCR coding sequence. The present sequence was derived from stromal stem cells. The present sequence and its corresponding protein are useful in the prevention, diagnosis and treatment of diseases associated with inappropriate 7TM-GPCR expression. TYM-GPCRs identify specific signalling molecules, to activate an effector signalling cascade that triggers an intracellular response and eventually a biological effect.
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                                          sequence #326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TTGAGAAGGTTCGCTCTGTCTTTGAAAGAGCCCTGTCCTCTGTTGGCCTGCACATGACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               619 TTGAGAAAGTTCGCTCCGTGTTTGAAAGGGCTCTCTCGTCTGTTGGTTTACATATGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          679 AAGGACTCGCCCTCTGGGAGGCTTACCGAGAGTTTGAAAGTGCGATTGTGGAAAGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       739 GGCTTGAGAAAGTCCACAGATCTTTTCCGGCGACAGTTGGCGATCCCACTCTATGATATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGCCACATTTGCAGAGTATGAAGAATGGTCAGAAGACCCAATACCAGAGTCAGTAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559 CTAACATTTGGCTAGAGTATGGCCAGTACTCAGTTGGTGGGATTGGTCAGAAAGGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                            DNB. Sequences encoding 7-transmembrane G-protein coupled protein receptors characteristic of hematopoietic stem cells, useful for treating leukemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                          Murine 7-transmembrane G-protein coupled receptor coding
                                                                         stromal stem cell; signalling; vaccine; 7TM-GPCR;
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                                                                                       7-transmembrane G-protein coupled protein receptor; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
9.1%; Score 346.8; DB 22;
Best Local Similarity 79.9%; Pred. No. 1.2e-83;
Matches 436; Conservative 0; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 143-144; 176pp; English.
                                                                                                                                                                                                                                                                                                                     Pereira DS;
                                                                                                                                                                                                             14-FEB-2001; 2001WO-US04700.
                                                                                                                                                                                                                                           14-FEB-2000; 2000US-0182377
                                                                                                                                                                                                                                                                           (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                     Lemischka IR, Witte L,
                                                                                                                                                                                                                                                                                         (UYPR-) UNIV PRINCETON
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                                                                                                                                                  WO200160999-A1,
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2000US-0230438
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20000S-0231243
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2000US-0246526
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05-SEP-2000)
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13-0CT-2000;
20-0CT-2000;
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14-SEP-2000;
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08-NOV-2000;
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25-SEP-2000
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29-SEP-2(
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                360 TGCAGGCAGANGNCCCTCGGCNGGCGGAATACCAAGCTTACATCGANTTCGAGATGAAAA 419
                                                                                                                                                                                                                     Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                    Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30602
                                                                                                                                               AAK75790 standard; DNA; 543 BP.
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2000US-0224519.
2000US-0225213.
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                                                                                                                                                                                    (first entry)
                                                                                    1099 TGGTTT 1104
                                                                                               537 TGGTTT 542
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18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
                                                                                                                                                                                                                                               Homo sapiens
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28-JUN-2000;
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393 GTGTTATCGCGGGCTGTGGCCGCTGCGACATACAAGACCATGGGGCCAGCGTGGGATCAG 334
                                       243 AGCTCCCCGGGGAGTACGAGTGGGAATATGACGAAGAGAGGAGAAAAACCAGCTGGAG
                            183 CAGGAGGAAGCCGTGAGCGAGAGCGATGGGGATGAGTACGCCATGGCTTCCTCCGCGGAG
                                                                                                                                                                                                                                                                                                                                              Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                  Human breast cell single exon nucleic acid probe #7826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W, Rank DR;
                                                                                                                                      303 ATTGAGAGACTGGAGGAGCAGTTG 326
                                                                                                                                                      213 ATTGAGAGACTGGAGGAGCAGGTG 190
                                                                                                                                                                                                                                    ABA49131 standard; DNA; 312 BP
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2000US-0234687
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                                                                                                                                                                                                                                                                                                                                                             disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                               WO200157271-A2
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27-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) acmino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to pulynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting protein. (I) proteins and polynucleotides may be used to produce the secreted diseases, especially cancers and concernmentalses of haematopoietic-related diseases, especially concernmentalses of haematopoietic-derived cells. AAK64703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 30602; 3071pp + Sequence Listing; English.
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Pred. No. 7.5e-75;
0; Mismatches 6; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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Best Local Similarity 98.1%;
Matches 318; Conservative
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encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a spatially-addressable set of single exon
New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               derived from mRNA of human breast, and then measuring the label
bound to each probe of the microarray. The probes are useful for
verifying the expression of regions of genomic DNA predicted to
                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 7826; 327pp + sequence listing; English.
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182

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Gaps

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ACGCGTCCGATGGCGACTGCGGCCGAAACCTCGGCTTCAGAACCCGAGGCTGAGTCCAAG

513 AAGCGCAAGATGGCGACTGCGGCCGAAACCTCGGCTTCAGAACCCGAGGCTGAGTCCAAG

GTGTTATCGCGGGCTGTGCGCCTGCGACATACAAGACCATGGGGCCCAGCGTGGGATCAG

GCTGGCCCCAAGGCTGACGGAGGAGGATGAGGTTAAGGCGGCTAGGACAAGGAGAAAG

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Gaps

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CGGGCTGTGGCCGCTGCGACATACAAGACCATGGGGCCAGCGTGGGATĆAGCAGGAGGAA 191
                                                                                                                                                                                                                                                                                                                                                                                                measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                 AAGGCTGACGGAGGAGGATGAGGTTAAGGCCGCTAGGACAAGGAGAAAGGTGTTATCG
                                                                                                                                                                                                                                                                                                              CGGGCTGTGGCCGCTGCGACATACAAGACCATGGGGCCAGCGTGGGATCAGCAGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                     GGGGAGTACGAGTGGGAATATGACGAAGAGGGGGGAGAAAAACCAGCTGGAGATTGAGAGA
                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                   GGCGTGAGCGAGAGCGATGGGGATGAGTACGCCATGGCTTCCTCCGCGGAGAGGCTCCCCC
                                                                                                                                                                                      12 ATGGCGACTGCGGCCGAAACCTCGGCTTCAGAACCCGAGGCTGAGTCCAAGGCTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #12604 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                     Score 310.4; DB 22; Length 312;
Pred. No. 6.5e-74;
); Mismatches 1; Indels 0;
                                                                                                               Sequence 312 BP; 41 A; 125 C; 66 G; 80 T; 0 other;
                                                                                                                                                 Pred. No. 6.5e
0; Mismatches
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ABA34138 standard; DNA; 312 BP.
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2000US-0207456.
2000US-0608408.
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2000US-0234687
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nes 311; Conservative
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                                                                                                                         ATGCCGACTGCGGCCGAAACCTCGGCTTCAGAACCCGAGGCTGAGGTCCAAGGCTGGGCCC
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                                                    Length 312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human foetal liver single exon nucleic acid probe #15350
                                                                          Indels
   from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                 8.2%; Score 310.4; DB 22;
99.7%; Pred. No. 6.5e-74;
ive 0; Mismatches 1;
                           Sequence 312 BP; 41 A; 125 C; 66 G; 80 T; 0 other;
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2000US-0608408.
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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                                                              al Similarity 99.7
311; Conservative
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30-JUN-2000;
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27-SEP-2000;
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                                                 Query Match
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Matches 311;
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Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
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Caim 4; SEQ ID No 12604; 530pp; English.
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CC
The present invention relates to single exon nucleic acid probes for
measuring human gene expression in a sample derived from human heart. The
CC measuring and displaying gene expression in samples for
predicting, measuring and displaying gene expression in samples derived
CC producting, measuring and displaying gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC congenital heart disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC Specification, but was obtained in electronic format directly from WIPO
XX
Sequence 312 BP; 41 A; 125 C; 66 G; 80 T; 0 other;
OUBLY MATCH

OUBLY MATCH

8.2%: Score 310.4: DB 22: Length 312:
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131
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                                                                                                                                                                                                              192 GGCGTGAGCGAGAGAGTGGGGATGAGTACGCCATGGCTTCCTCCGCGGAGAGCTCCCCC 251
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                                                       71
                                                                                                                                                                                                                                                                               72 AAGGCTGACGGAGGAGGATGAGGTTAAGGCGGCTAGGACAAGGAGAAAGGTGTTATCG
                                                                                                                                                                                                                             12 ATGGCGACTGCGGCCGAAACCTCGGCTTCAGAACCCGAGGCTGAGGCTGGGCCC
                            0; Gaps
    Length 312;
Score 310.4; DB 22; Length
Pred. No. 6.5e-74;
0; Mismatches 1; Indels
Query Match 8.2%;
Best Local Similarity 99.7%;
Matches 311; Conservative
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Search completed: June 22, 2003, 07:08:46 Job time : 535 secs 20, Appl 20, Appl 20, Appl 6, Appli 205, App

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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
         US-09-256-976-16
US-08-728-334-1
US-08-728-58-1
US-08-770-379-20
US-08-770-379-20
US-09-078-294-6
US-09-078-294-6
US-09-461-697-203
US-09-461-697-193
US-09-461-697-189
US-09-461-697-189
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US-09-461-697-187
US-09-461-697-185
US-09-461-697-184
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F.
APPLICANT: SCHETELINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
                                                                                                                                                                                                                                                                 US-08-314-503A-1
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REFERENCE/OCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 91 114 300.
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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9171.326 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                       ; Search time 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      - nucleic search, using sw model
                                                                                                     June 22, 2003, 06:58:01
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Maximum DB seq length: 200000000
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Match 1
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Perfect score:
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Length 7218;

DB 1;

2.5%; Score 95.6;

STRANDEDNESS: single

Sequence

-US93-04648-15

Sequence

Sequence Sequence Sequence Sequence

US-08-834-306-16 -317-844B-1

linear

, CLONE: pTZgpt-Fls US-08-232-463-14

Query Match

IMMEDIATE SOURCE:

Genes

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GAGGAGAAAAACCAGCTGGAGATTGAGAGACTGGAGGAGCAGTTGTCTATCAACGTCTAT 341
                                                                                                           42 GAACCCGAGGCTGAGTCCAAGGCTGGGCCCAAGGCTGACGGAGGAGGAGGATGAGGTTAAG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 GAGGAGAAAAACCAGCTGGAGATTGAGAGACTGGAGGAGCAGTTGTCTATCAACGTCTAT 341
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                                                                                                                                                                                                                                                                                                         APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing of TITLE OF INVENTION: From Multiple Transfected Episomes FILE REFERENCE: 0867/10903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEO ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 57.8; DB 2;
Pred. No. 7.6e-06;
0; Mismatches 202;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                  GACGGGGACGGGGAGGAG 533
                                                                                                                                                  GTGAGGATGGCCCGCCAGAAG 422
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Patent No. 5976807
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Best Local Similarity
Matches 179; Conserv
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US-09-397-787-257
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                                                                                                                                                                                                                                              GAGAAGAAGCGTTAAAAAGAAGAAAAAGATCAGAGCCCCAGAGAAGCGCGGGGCAGAT 1889
                                                                                                                                                                                                                                                                                                           GAGGACGATGAGAAAGAGTGGGGCGATGATGAAGAAGAGCCAGCACTTCCAAACGCAGAAGG 1949
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                                                                                                                                      1650 GAAGTGTTACTCACCATGGAGGACAGAAGGTTCTTTAGAAGATTGGGATATAGCTGTT
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                    Gaps
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Patent No. 6417002
GENERAL INFORMATION:
APPLICANT: Horlick, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/00905
CURRENT FILIAG DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
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     Pred. No. 5.4e-16;
5; Mismatches 124;
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Pred. No. 7.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature

: LOCATION: (1)...(1926)

: OTHER INFORMATION: template strand of EBNA-1 DNA

US-09-249-585A-4
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Best Local Similarity 4.3%; Pre
Matches 17; Conservative 255;
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ORGANISM: Epstein Barr Virus
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Best Local Simi:
Matches 179;
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us-09-763-985a-1.rni

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133 GGGCTGTGGCCGCTGCGACATACAAGACCATGGGGCCAGCGTGGGATCAGCAGGAGGAAG 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/676,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Science & Technology Law Group STREET: 268 Bush Street, Suite 3200 CITY: San Francisco
                  240052.419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08676967
Patent No. 5747317
GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INPORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 51259 base pairs
TYPE: nucleic acid
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NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36,627
39,317
                  REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (415)343-4342
                                                                                                                                                                                                                                                          Query Match 1.3
Best Local Similarity 49.8
Matches 125; Conservative
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                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     1.4%; Score 51.4; DB 4; Length 436; 51.1%; Pred. No. 0.00018; Live 0; Mismatches 116; Indels
              APPLICANT: Lodes, Michael J.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS
FILLE REFERENCE: 21012.46662
CURRENT APPLICATION NUMBER: US/09/397,787
CURRENT FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 334
SEQ ID NO 257
LENGTH: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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6300 Columbia Center, 701 Fifth Avenue
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NAME: No. 6090620tenburg Ph.D., Carol
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                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LCCATION: (1)...(436)
; OTHER INFORMATION: n = A,T,C or G
US-09-397-787-257
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Yu, Chang-En
Oshima, Junko
Benson, Darin R.
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapien
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Matches 121; Conserv
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2467 AAATCTGTAAGGCTCATGGCACCGTGAAGGACCTCAGGCTGGTCACCAACCGGGCTGGCA 2526
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                                                                           395 CNGTNTTYGCNCARTTYGGNGCNGTNYTNGARGTNAAYATHCCNMGNAARCCNGAYGGNA
                                                                                                                                                            2527 AACCAAAGGGCCTGGCCTACGTGGAGTATGAAATGAATCCCAGGCGTCGCAGGCTGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09098487
Patent No. 5917025
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ATTORNEY/AGENT INFORMATION:
NAME: OSMAN Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB9
TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
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; MOLECULE TYPE: CDNA
US-09-098-487-2
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US-09-098-487-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              455 ARATGMGNGGNTTYGGNTTYGTNCARTTYAARAAYYTNYTNGARGCNGGNAARGCNYTNA 514
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                                                                                                                                                            Length 2277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2587 TGAAGATGGACGCATGACTATCAAAGAGAACATCATCAAAGTGG 2631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          515 ARGGNATGAAYATGAARGARATHAARGGNMGNACNGTNGCNGTNG 559
                                                                                                                                                                                                                       36; Mismatches 115; Indels
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                                                                                                                                                            Score 47.6;
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Patent No. 5770422

GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UCB96-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: UC
                                                                                                                                                         1.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.9%;
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Best Local Similarity 32.>>
المالية المال
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                                                                                                                                                         Query Match 1.3°
Best Local Similarity 32.9°
Matches 74; Conservative
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double
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                             ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-676-967-2
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   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                            Sequence 17, Application US/09007005B
Fatent No. 625858
GENERAL INPORMATION:
APPLICANT: Scotak, Jack W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: ENSIONS
FILE REFERENCE: 00786/350003
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/005,963
EARLIER APPLICATION NUMBER: 60/005,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-06
SEALIER FILING DATE: 1997-01-06
SOFTWARE: FESE OF OF WINDOWS VERSION 4.0
SEQ ID NO 17
LENGTH: 289
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APPLICANT: SZOSTAK, JACK W.
APPLICANT: LAUGENTS, Richard W.
APPLICANT: Liu, Richard W.
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: PUSIONS
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT APPLICATION NUMBER: 05.05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.2%; Score 47.4; DB 4; Length 2
Best Local Similarity 6.9%; Pred. No. 0.0019;
Matches 17; Conservative 112; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Translation template
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LCCATION: (1)...(289)
COTHER INFORMATION: n = A,T,C or G
US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Artificial Sequence
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US-09-244-796-17
SULT 9
-09-007-005-17
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1748 GAGAATGAAGGCTGCAGAAGGAAGCAGCCCTTGTGCAGCAAGAAGAAAAAAGGCTGA 1807
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Patent No. 6417002
GENERAL INFORMATION:
APPLICANT: HOTLICK, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
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Pred. No. 0.0059;
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Best Local Similarity 6.9%; Pred. No. 0.0019;
Matches 17; Conservative 112; Mismatches 118;
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EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                 : NAME/KEY: misc_feature

: LOCATION: (1)...(289)

: OTHER INFORMATION: n = A,T,C or G

US-09-244-796-17
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Best Local Similarity 43.4%;
Matches 219; Conservative (
                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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ORGANISM: Epstein Barr Virus
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MOLECULE TYPE:
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US-09-050-863-2
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                           GCCATGGCTTCCTCCGCGGAGAGCTCCCCCGGGGAGTACGAGTGGGAATATGACGAAGAG
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                                                       ATGGGGCCAGCGTGGGATCAGCAGGAGGAGGCGTGAGCGAGAGCGATGGGGATGAGTAC
                                                                                                                                        402 GTGAGGATGGCCCGCCAGAAGATGAGTGAAATCTTTCCCTTGACTGAAGAGCTCTGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Mammalian Protein Interaction Cloning TITLE OF INVENTION: System NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elehr, Hohbach, Test, Albritton & Herbert & Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: $11va, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
                                                                                                                                                                                                                                                                                                                                                                                                              522 GACCTCTTTGAGAAGCCGTGAAGG 546
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30-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible OPERATING SYSTEM PC-DOS/MS-DOS SOFTWARE: PAtentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09050863
Patent No. 6114111
GENERAL INFORMATION:
APPLICANT: Lao, Ying
APPLICANT: Hlang, Betty
APPLICANT: Payan, Don
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 941-1989
TELEFAX: (415) 949-8711
FORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2580 Decree
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION
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TOPOLOGY: un
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STREET: 4 E
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                                                                                                                                                                                                                                   162 ATGGGGCCAGCGTGGGATCAGCAGGAGGAAGGCGTGAGCGAGAGCGATGGGGATGAGTAC
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                                        Gaps
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ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Mammalian Protein Interaction
System
                              0; Mismatches 286;
  3;
Score 47.4; DB Pred. No. 0.007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,081
FILING DATE: 22-Jul-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/050,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    522 GACCTCTTTGAGAAAGCCGTGAAGG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09359081
Patent No. 6316223
GENERAL INFORMATION:
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STATE: CA
  1.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hiang, Betty.
Payan, Don
Query Match 1.29
Best Local Similarity 43.49
Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lao, Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCES:
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                               ORGANISM: VEBNA
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                                 5452
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                                                                               US-09-130-114-1
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                                                 TYPE: DNA
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                  SEQ ID NO 1
                                                                                                               Query Match
Best Local
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APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Enkaryotic Cells Stably Expressing Genes
FILLE REFERENCE: 0867/1D903US1
                                                                                                                                                                                                                                                                                                                    Indels
                             NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
                                                                                                                                                                                                                                                                                    Score 47.4; DB 4; 1
Pred. No. 0.007;
0; Mismatches 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 0867/ID903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                      ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-359-081-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1390 GCCGGGGTCGAGGAGGTAGTGGAGG 1414
                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  522 GACCTCTTTGAGAAGCCGTGAAGG
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Patent No. 5976807
GENERAL INFORMATION:
                                                                                                                                                      LENGTH: 2580 base pairs
                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                   Query Match 1.2%;
Best Local Similarity 43.4%;
Matches 219; Conservative
                                                                                                                                                                                                          TOPOLOGY: unknown
FILING DATE:
                                                                                                                                                                                                                         MOLECULE
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                                                                                   42 GAACCCGAGGCTGAGTCCAAGGCTGGGCCCCAAGGCTGACGGAGGAGGATGAGGTTAAG
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    Length 5452;
                                              Indels
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APPLICATION NUMBER: US/08/910,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \mathbf{for}
Score 47.4; DB 2;
Pred. No. 0.011;
0; Mismatches 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08910647
Patent No. 6251433
GENERAL INFORMATION:
GENERAL INFORMETION:
TITLE OF INVENTION: Compositions and Method
TITLE OF INVENTION: Polynucleotide Delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              522 GACCTCTTTGAGAAAGCCGTGAAGG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Chiron Corporation
STREET: 4560 Horton Street
    1.28;
                          43.48;
                                              Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 94608-2916
COMPUTER READABLE FORM:
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                          Similarity
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162 ATGGGGCCAGCGTGGGATCAGCAGGAGGCGTGAGCGAGGCGAGGGGATGGGGATGAGTAC 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402 GTGAGGATGCCCCGCCAGAAGATGAGTGAAATCTTTCCCTTGACTGAAGAGCTCTGGCTG 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 462 GAGTGGCTGCATGACGAGATCAGCATGGCCCAGGATGGCCTGGACAGAGAGCACGTGTAT 521
                                                                                                                                                                                                                                                                                                                                                                                                   42 GAACCCGAGGCTGAGTCCAAGGCTGGGCCCAAGGCTGACGGAGAGGAGGATGAGGTTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 GCGGCTAGGACAAGGAGAAAGGTGTTATCGCGGGCTGTGGGCCGCTGCGACATACAAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342 GACTACAACTGCCATGTGGACTTGATCAGACTGCTCAGGCTGGAAGGGGAGCTTACCAAG
                                                                                                                                                                                                                                                                                                                       Score 47.4; DB 4; Length 9600;
Pred. No. 0.016;
0; Mismatches 286; Indels 0
                  NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
RELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9600 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-910-647-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           522 GACCTCTTTGAGAAAGCCGTGAAGG 546
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Best Local Similarity 43.4%;
Matches 219; Conservative
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
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Search completed: June 22, 2003, 09:53:52 Job time : 129 secs

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(without alignments)
16107.770 Million cell updates/sec
                                                                                                                                                                   June 22, 2003, 08:55:51; Search time 346 Seconds
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                            1042519 seqs, 733713590 residues
                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                           IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                      Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                             Scoring table:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

/ cgn2_6/ptodata/2/pubpna/USO7_pUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/NCS06_PUBM_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO6_PUBM_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:* Published_Applications_NA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 30, Appl	Sequence 556, App	Sequence 7319, Ap	Sequence 27590, A	Sequence 1728, Ap	Sequence 2028, Ap	Sequence 19458, A	Sequence 2624, Ap	Sequence 2624, Ap	Sequence 6818, Ap	Sequence 6818, Ap	Sequence 2742, Ap	Sequence 18092, A	Sequence 1331, Ap	Sequence 22608, A	Sequence 20733, A	Sequence 89, Appl	Sequence 3972, Ap	Sequence 69, Appl	
B ID	10 US-09-821-883-30	10 US-09-925-300-556	9 US-09-764-891-7319	9 US-09-918-995-27590	10 US-09-867-701-1728	10 US-09-867-701-2028	10 US-09-864-761-19458	9 US-09-796-692-2624	9 US-10-040-862-2624	9 US-09-796-692-6818	9 US-10-040-862-6818	10 US-09-864-761-2742	10 US-09-864-761-18092	10 US-09-864-761-1331	10 US-09-864-761-22608	10 US-09-864-761-20733	9 US-10-002-344A-89	10 US-09-864-761-3972	9 US-10-101-487-69	
å Query Match Length DB	3537	3355	32145	267	432	430	312	284	284	244	244	475	185	467	272	575	1282	1969	554	
% Query Match	76.0	67.5	27.8	11.6	10.4	10.3	8.2	7.5	7.5	6.4	6.4	5.8	3.4	3.3	1.5	1.5	1.5	1.5	1.4	
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Sequence 106, App Sequence 5848, Ap	Sequence 153, App	Sequence 29013, A	Sequence 10, Appl	Sequence 71, Appl	Sequence 73, Appl	Sequence 20, Appl	Seguence 1, Appli	Sequence 74, Appl	Sequence 76, Appl	Sequence 19707, A	Sequence 2926, Ap	Sequence 21553, A	Seguence 7684, Ap	Sequence 250, App	Sequence 256, App	Sequence 887, App	Sequence 937, App	۷.	Sequence 255, App	Sequence 886, App	Sequence 933, App	Sequence 14, Appl	Sequence 2218, Ap
US-10-101-487-106 US-09-864-761-5848 US-09-876-889-257	US-09-244-694-153	US-09-918-995-29013	US-10-123-155-10	US-10-101-487-71	US-10-101-487-73	US-09-771-208-20	US-10-067-514-1	US-10-101-487-74	US-10-101-487-76	US-09-864-761-19707	US-09-864-761-2926	US-09-864-761-21553	US-09-864-761-7684	US-10-091-438-250	US-10-091-438-256	US-09-764-853-887	US-09-764-853-937	US-10-091-438-246	US-10-091-438-255	US-09-764-853-886	US-09-764-853-933	US-10-291-230-14	US-09-864-761-2218
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ALIGNMENTS

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ULT 1 09-821-883-30 acquence 30. Application US/09821883 acquence 30. Application US/09821883 acquence 30. Application US/09821883 acquence 30. Application US/09821883 acpricANT: Laus, Reiner APPLICANT: Used and Methods for Dendritic TITLE OF INVENTION: Compositions and Methods for Dendritic TITLE OF INVENTION: Cell-Based Immunotherapy TITLE OF INVENTION: Cell-Based Immunotherapy TITLE OF INVENTION: Cell-Based Immunotherapy CURRENT APPLICATION NUMBER: US/09/821,883 CURRENT FILING DATE: 2000-03-30 CURRENT APPLICATION NUMBER: US 60/193,504 NUMBER OF SEQ ID NOS: 30 SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 30 ELENCTH: 3537 TYPE: DNA ORGANISM: Artificial Sequence FRATURE: OTHER INFORMATION: SART-3-IC	Score 2886; Pred. No. 0; 0; Mismatches	TCGGCT TCGGCT	GAGGTT GAGGTT	TACAAG TACAAG	GATGAG
UUT 1 09-821-883-30 acedence 30, Application US/09821 atent No. US20020061310a1 ENERAL INFORMATION: APPLICANT: Laus, Reiner APPLICANT: Graddis, Thomas APPLICANT: Graddis, Thomas TITLE OF INVENTION: Compositions TITLE OF INVENTION: Compositions FILE REPERENCE: 7636-0022.30 CURRENT APPLICATION NUMBER: US/0 CURRENT FILING DATE: 2001-03-30 PRIOR APPLICATION NUMBER: US 60/ PRIOR APPLICATION NUMBER: US 60/ PRIOR APPLICATION NUMBER: US 60/ PRIOR PRILING DATE: 2000-03-30 WUMBER OF SEQ ID NOS: 30 ENGWARE: FRASEQ for Windows Ve EQ ID NO 30 LENGTH: 357 TYPE: DNA ORGANISM: Artificial Sequence PEATURE INFORMATION: SART-3-IC 09-621-883-30	% 0 %	AAACC 	AGGAT	CGACA	ATGGG
ULT 1 09-821-883-30 equence 30, Application US/098: atent No. US20020661310A1 ENERAL INFORMATION: APPLICANT: Laus, Reiner APPLICANT: Graddis, Thomas TITLE OF INVENTION: Composition TITLE OF INVENTION: Cell-Base FILE REFERENCE: 7636-002.30 CURRENT APPLICATION NUMBER: US, CURRENT APPLICATION NUMBER: US, PRIOR APPLICATION NUMBER: US, PRIOR APPLICATION NUMBER: US, COURRENT FILING DATE: 2000-03-30 NUMBER OF SEQ ID NOS: 30 EQ ID NO 30 ELENCIH: 3537 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: SART-3-IC	76.0%; 100.0%; ative	000000	GAGAGO 	CCGCTG	AGAGCG
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ULT 1 09-821-883-30 cequence 30, Application of a tent No. US20020061310A1 ENERAL INFORMATION: APPLICANT: Laus, Rether APPLICANT: Caddis, Thon TITLE OF INVENTION: Cemportance of INVENTION: Cemporter APPLICATION UNMBECURRENT APPLICATION NUMBER OF SEQ ID NOS: 30 NUMBER OF SEQ ID NOS: 30 CURRENT FILING DATE: 2000-(NUMBER OF SEQ ID NOS: 30 NUMBER OF SEQ ID NOS: 30 LENGTH: 3537 TYPE: DNA ORGANISM: Artificial Sec FEATURE: ATTIFICIAL SEC TON SERVICE: CONGRANISM: ATTIFICIAL SEC SEGANISM: ATTIFICIAL SEC SEC SEGANISM: ATTIFICIAL SEC SEC SEGANISM: ATTIFICIAL SEC	Simila 6; Cc	ATGGC ATGGC			GGCGI
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RESULT 1 US-09-821-883-30 Sequence 30, Application US/09821883 Patent No. US20020061310A1 GENERAL INFORMATION: APPLICANT: Laus, Reiner APPLICANT: Graddis, Thomas TITLE OF INVENTION: Compositions an TITLE OF INVENTION: Compositions an TITLE OF INVENTION: Compositions an TITLE OF INVENTION: Coll-based Imm FILE REFERENCE: 7636-0022.30 CURRENT APPLICATION NUMBER: US/09/8 CURRENT FILING DATE: 2001-03-30 PRIOR PAPLICATION NUMBER: US 60/193 PRIOR FILING DATE: 2000-03-30 NUMBER: FastSEQ for Windows Versi SOFTWARE: FastSEQ for Windows Versi SOFTWARE: ATTYPE: DNA ORGANISM: Artificial Sequence FFATURE: COTHER INFORMATION: SART-3-IC	Ouery Match Best Local Similarity 100. Matches 2886; Conservative				
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Oy 2412 CACAAGCTGTTCATCTCAGGCCTGCCTTTCTCCTGTACTAAAGAGGAACTAGAAGATC 2471 Dh 2401 [11] [11] [11] [11] [11] [11] [11] [1	Oy 1265 GGAGATTTGGCAGGCATACČTT 	GAGATTTGGCAGGCATACĊTTGATTACCTGAGGAGGAAGGGTTGATTTCAAACAACACTC 1324
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; Sequence 556, Application US/09925300 ; Patent No. US20020151681A1 ; GENREAL INFORMATION:	OY 1865 AGCCCAGAGAAGCGCGGAGCP	AGGCCCAGAGAAGCGCGGAGCAGATGAGACGATGAGAAAGAGTGGGGCGATGATGAAGA 1924
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REPERENCE: PAID FILE PROFESSION: MANAGED ACIDS, Proteins and Antibodies FILE PROFESSION: AND TANKAN MINISTER ACIDS ACCORDING ACIDS	OY 1925 AGAGCAGCCTTCCAAACGCAGA	AGAGCAGCCTTCCAAACGCAGAAGGGTCGAGAACAGCATCCCTGCAGCTGGAGAAACACA 1984
CORRENT FILING DATE: 05/03/925.500 PRIOR APPLICATION NUMBER: PCT/USO0/05988 PRIOR FILING DATE: 2000-03-08 PRIOR FILING DATE: 2000-03-08 PRIOR FILING NUMBER: PCT/USO0/05988	. 0y 1985 AAATGTAGAAGTAGCAGGAGGAGGAGGAGGAGGAGGAGAGAGA	AAATGTAGAAGTAGCAGGCCCCGCTGGGAAATGTGCTGCCGTAGATGTGGAGCCCCC 2044
FALSA REFLICATION WORDER: 00/124,2/0 ; PRIOR FILING DATE: 1999-03-12 ; NUMBER OF SEQ ID NOS: 1890 ; SOFTWARE: PetentIn Ver. 2.0	Qy 2045 TTCGAAGCAGAAGGAGAGGCA 	TCGAAGCAGAAGGAAGCCAGCCTCCCTGAAGAGGACATGCCCAAGGTGCTGCACGA 2104
	Oy 2105 CAGCAGCAAGGACAGCATCACC	CAGCAGCAAGGACAGCATCACCGTCTTTGTCAGCAACCTGCCCTACAGCATGCAGGAGCC 2164
; FANDORE: misc feature ; DOCATION: (210) ; OTHER INFORMATION: n equals a,t,g, or.c US-09-925-300-556	Oy 2165 GGACACGAAGCTCAGGCCACTC	GGACACGAAGCTCAGGCCACTCTTCGAGGCCTGTGGGGAGGTGGTCCAATCCGACCAT 2224
Query Match Query Match G7.5%; Score 2563.2; DB 10; Length 3355; Best Local Similarity 99.8%; Pred. No. 0; Matches 2576; Conservative 0; Mismatches 3; Indels 1; Gaps 1;	Oy 2225 CTTCAGCAACCGTGGGGATTTC 	CTTCAGCAACCGTGGGGATTTCCGAGGTTACTGCTACGTGGAGTTTAAAGAAGAAATC 2284
AACCTTGAGAAAGCTTTGAATGCCGGCTTCATCTGGGCCACTGATTATGT 12 AACTTGAGAAAGCTTTGAATGCCGGCTTCATCAGGCCACTGATTATGT 44	Qy 2285 AGCCTTCAGGCACTGGAGATG	AGCCCTTCAGGCACTGGAGATGGACCGGAAAGTGTAGAAGGGAGGCCAATGTTTGTT
** 191011091909990099109119999999109111991109999109999109999	Qy 2345 CCCTGTGTGGATAAGAGCAAA	CCCCTGTGTGGATAAGAGCAAAAACCCCGATTTTAAGGTGTTCAGGTACAGCACTTCCCT 2404

Db 2606 TITITATATTATGTATATGTAAATGACATGTCAGCCCTTGTTTCATGTTTCCTAAAAGCA 2665 Qy 3484 GAATATTGCAACATTTGTATAGGAATTATTTGTCCCACCTGCTGGACTGTTT 3543	RESULT 3 US-09-764-891-7319 is Sequence 7319, Application US/09764891 is Sequence 7319, Application US/09764891 is Dublication No. US20030077808A1 is GENERAL INFORMATION: is APPLICANT: ROSEN et al. if TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies if TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies if CURRENT PELING DATE: 2001-01-17 is CURRENT FILING DATE: 2001-01-17 is Prior application data removed - consult PALM or file wrapper is NUMBER OF SEQ ID NOS: 10231 is SOFTWARE: PatentIn Ver. 2.0 is SEQ ID NO 7319 iLENGTH: 32145 iLENGTH: 32145 if YPE: DNA incomplement of the prior of the prior of the wrapper of the prior of the wrapper incomplement	27.8%; Score 1056.4; DB 9; Length 32145; 57. Conservative	Db 23920 CACCGAGGCACCCAAGATGTCCAATTTGCCAAGCTTTTGGCAAAGTGAAC 23979 Oy 2906 GGGACGCTGGGAAATGCCTTACTTCACTCTGGCCCGCGCACCCCCCCC
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                                          26 GTGCAACTCGAAATGCCTTACTTCACTCTGGCCCGGGGGACCTCCCACCACCACCAGCAGTG
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE:
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.49 CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FESTERE for Windows Version 4.0
SEQ ID NO 1728
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Patent No. US2002013237A1
GENERAL INFORMATION:
APPLÏCANT: Aglate, Paul A.
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                            TTGAGACACAGTTGTCCAAATGTTTCTGGCCAGCTCCGGCCCCTTTTTGTATGACACTTC
                                                                                  TCTTCCACCCTGCACAGCACATGTGCCGTCATTCTTTTAATTTTAAAAGATGAAATGGC
                                                                                                                                                      24340 TCTTCCACCCTGCACAGCACATGTGCCCGTCATTCTTTAATTTTAAAAGATGAAATGGC
                                                                                                                                                                                    AAAACATTTGCTGGAGTTTTGTTCAATGGGGCTGTGCATTTTTATATATGTGTTTGTAA
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Pred. No. 3.2e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES (TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/255,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 38054
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27590
LEMCTH: 567
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Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(567)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-27590
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98.2%;
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXPRESSION ANALYSIS BY MICROARRAY FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY CURRENT APPLICATION NUMBER: US/09/864,761 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR P
   3363 TGGGTCTGAGGGAAGTCAGCTATAAAACATTTGCTGGAGTTTTGTTCAATGGGGCTGTGC 3422
                                                                                                                                                 3423 ATTTTT-ATATTATGTGTTTGTAAATGACATGTCAGCCCTTGTTTCATGTTTCCTAAAAG 3481
                                             300 TGGGTCTGAGGGAAGTCAGCTATAAAACATTTGCTGGNGTTTTGTTCATCAGGGGCTGTGC 359
                                                                                                                                                                                       OTHER INFORMATION: MAP TO AC008119.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.9
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PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-06-03
PRIOR PELICATION NUMBER: US 09/632,366
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-07
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
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Patent No. US20020048763A1
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PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Adjate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
APPLICANT: Harlocker. Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 210121.497
CURRENT APPLICATION UNDBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: EsetSEQ for Windows Version 4.0
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llarity 98.8%; Pred. No. 3.5e-110;
Conservative 0; Mismatches 2; 1
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Patent No. US20020132237A1
GENERAL INFORMATION:
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; LCCATION: (1)...(430)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-2028
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ORGANISM: Homo sapien
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Matches 426; Conserv
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APPLICANT: GA194: Alexander
APPLICANT: GA194: Alexander
APPLICANT: Bacter: Marc
APPLICANT: Retter: Marc
APPLICANT: Retter: Marc
APPLICANT: Retter: Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
TITLE OF INVENTION: Hematological Malignancies
CURRENT TILING DATE: 2001-11-06
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR PRIOR APPLICATION NUMBER: US 60/206, 201
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-07-14
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100.0%; Pred. No. 7.7e-77;
iive 0; Mismatches 0;
  PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FASTERO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2624, Application US/10040862 Publication No. US20030078396A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                         284; Conservative
                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-09-796-692-2624
                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                  LENGTH: 284
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APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
TYPLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: 05/196/5622
CURRENT APPLICATION NUMBER: 60/186/126
PRIOR APPLICATION NUMBER: 60/180/479
PRIOR FILING DATE: 2000-03-01
PRIOR PELING DATE: 2000-03-17
PRIOR PELING DATE: 2000-04-27
PRIOR PELING DATE: 2000-04-28
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                                                N: EXPRESSED IN PLACENTA, SIGNAL = 3.2

N: EXPRESSED IN HELA, SIGNAL = 4.3

N: EXPRESSED IN HEARY, SIGNAL = 2.6

N: EXPRESSED IN HEARY, SIGNAL = 3.5

N: EXPRESSED IN HEARY, SIGNAL = 3.4

N: EXPRESSED IN BRAIN, SIGNAL = 3.4

N: SWISSPOT HIT: P27476, EVALUE 0.00e+00

N: FIT: D63879.1, EVALUE 0.00e+00

N: EST_HUMAN HIT: BF514110.1, EVALUE 0.00e+00
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99.7%; Pred. No. 5.8e-85;
live 0; Mismatches 1
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Publication No. US20020198362A1
GENERAL INFORMATION:
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FILING DATE: 2000-05-22
APPLICATION NUMBER: 60/218,950
FILING DATE: 2000-07-14
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                            EXPRESSED
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          EXPRESSED
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Matches 311; Conservative
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TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-01324048
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR PELING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR PILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
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                                                                                                                                                                                                                                                                                                                        Query Match 6.4%; Score 244; DB 9; 1
Best Local Similarity 100.0%; Pred. No. 1.5e-64;
Matches 244; Conservative 0; Mismatches 0;
                        PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6818
LENGTH: 244
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PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
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PRIOR APPLICATION NUMBER: US 60/200,999
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PRIOR APPLICATION NUMBER: US 60/223,416
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PRIOR APPLICATION NUMBER: US 60/202,084
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FILING DATE: 2000-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6818, Application US/10040862 Publication No. US20030078396A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-05-22
                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-796-692-6818
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US-10-040-862-6818/c
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APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion: Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: OWNER: US/09/796,692
CURRENT FILING DATE: 2000-03-01
PRIOR PELICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-17
PRIOR PELING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-29
PRIOR PLING DATE: 2000-04-29
PRIOR FILING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-06-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR PLING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR PRIOR PLING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR PRIOR PRIOR DATE: 2000-05-22
PRIOR PRIOR PRIOR PRIOR DATE: 2000-05-22
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 284;
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  PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR ELILING DATE: 2000-08-07
PRIOR PLICATION NUMBER: US 60/223,378
PRIOR PLICATION NUMBER: US 09/796,692
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR PILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SEQ ID NO 2624
LENGTH: 284
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FILING DATE: 2000-07-14
FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.5
Best Local Similarity 100.
Matches 284; Conservative
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US-10-040-862-2624
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
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OTHER INFORMATION: MAP TO ALUCELONE MARNUW, C. OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.9

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 3.8

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN HEATO, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN HEATO, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN HEATO, SIGNAL = 3.5
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 2742
LENGTH: 475
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Best Local Similarity 99.13
Matches 221; Conservative
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US-09-864-761-18092/c
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Tence, Wensheng
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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                                                                                                                                                                                                                                                                                                                                                                6.4%; Score 244; DB 9; 100.0%; Pred. No. 1.5e-64; tive 0; Mismatches 0;
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6818
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PRIOR APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PLING DATE: 2000-02-04
PRIOR PLING DATE: 2000-02-04
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-06-05
PRIOR PLING DATE: 2000-06-03
PRIOR PLING DATE: 2000-06-03
PRIOR PLING DATE: 2000-06-03
PRIOR PLING DATE: 2000-06-03
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-07
PRIOR PLING DATE: 2000-10-07
PRIOR PLING DATE: 2000-01-07
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00664
PRIOR PLING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 244; Conservative
                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-6818
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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IN BRAIN, SIGNAL = 1.6

IN ADDLT LIVER, SIGNAL = 1.2

IN PLACENTA, SIGNAL = 1.9

JIN LUNG, SIGNAL = 1.4

JIN BONE MARROW, SIGNAL = 1.2

D IN FETAL LIVER, SIGNAL = 1.8

SI IN FTAY, SIGNAL = 1.5

TO IN FTAY, SIGNAL = 1.5
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 1331
LENGTH: 467
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00668
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PRIOR APPLICATION NUMBER: US 60/180,312
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
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PRIOR APPLICATION NUMBER: US 60/207,456
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PRIOR APPLICATION NUMBER: US 09/632,366
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                                                                                                                         Sequence 1331, Application US/09864761
Patent No. US20020048763A1
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OTHER INFORMATION:
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NY EXPRESSED IN ADULT LIVER, SIGNAL = 1.2

NY EXPRESSED IN LUNG, SIGNAL = 1.9

NY EXPRESSED IN LUNG, SIGNAL = 1.4

NY EXPRESSED IN FETAL LIVER, SIGNAL = 1.2

NY EXPRESSED IN BETAL LIVER, SIGNAL = 1.5

NY EXPRESSED IN HETAL, SIGNAL = 1.5

NY EXPRESSED IN HEART, SIGNAL = 1.5

NY EXPRESSED IN HEART, SIGNAL = 1.5

NY EXPRESSED IN HELA, SIGNAL = 1.7

NY EXPRESSED IN HELA, SIGNAL = 1.9

NY EXPLANTAL EXPLANTAL = 1.9

NY EXPLANTAL EXPLANTAL = 1.9

NY EXPLANTAL EXPLANTAL = 1.9
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: Annomax Sequence Listing Engine vers. 1.1
FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                   FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
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APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: US 09/608,408
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      914 ACTG 917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-864-761-18092
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                                                                                                                                                                                                                                                                                                                                                    1.5%; Score 55.6; DB 10; Length 272;
53.2%; Pred. No. 2.6e-06;
tive 0; Mismatches 104; Indels 0
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                                                                                                                                                INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2 INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2 INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2 INFORMATION: EXPRESSED IN HERA, SIGNAL = 1.7 INFORMATION: EXPRESSED IN HEARIN, SIGNAL = 2.3 INFORMATION: NT HIT: ABO19788.1, EVALUE 8.70e+00
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Job time : 350 secs
                                                       TO AC002539.1
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Matches 118; Conservative
ORGANISM: Homo sapiens
                                                    OTHER INFORMATION:
                                                                                                                             INFORMATION:
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US-09-864-761-22608
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PPLICANT: Chen, Wensheng
TILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                          382
                                                                                                                                                                                                                      792 GATATGGAGGCCACATTTGCAGAGTATGAAGAATGGTCAGAAGACCCAATACCAGAGTCA
                                                                                                                                                       Gaps
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                  Query Match 3.3%; Score 126.4; DB 10; Length 467; Best Local Similarity 99.2%; Pred. No. 5.3e-28; Matches 127; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/23,66
PRIOR PRILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00666
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FILING DATE: 2001-01-30
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PRIOR PEDLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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Patent No. US20020048763A1
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by T cells 3, clone IMAGE:5534381, mRNA.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Strausberg,R.
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Submitted (06-JON-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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Contact: MGC help desk
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                            16154066 seqs, 8097743376 residues
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Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
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                                                                                                                                             Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 69 Row: k Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gl: 7661951 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
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/clone_lib="NIH_MGC_71"
/lab_host="DH10B"
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Pred. No. 0;
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0; Mismatches
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llarity 99.7%;
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	61 AGGCTGGGCCCAAGGCTGACGAGAGGAGGATGAGGTTAAGGCGGCTAGGACAAGAGAAA 120 	121 AGGTGTTATCGCGGGCTGTGGCCGCTGCGACATACAAGACCATGGGGCCACCGTGGGGATC 180 111111111111111111111111111111111	181 AGCAGGAGGAGGGTGAGCGAGGCGATGGGATGAGTACGCCATGGCTTCCTCCGCGG 240	241 AGAGCTCCCCGGGGAGTACGAGTGGGAATATGACGAAGAGAGGAGGAAAAACCAGCTGG 300	AGATTGAGAGACTGGAGGAGGAGTTGTCTATCAACGTCTATGACTACAACTGCCATGTGG	ACTTGATCAGACTGCTCAGGCTGGAAGGGAGGTTACCAAGGTGAGGATGGCCCGCAAAALIIIIIIIIIIIIIIIIIIIIIIIIIIII	AGATGAGTGAAATCTTTCCCTTGACTGAAGAGCTCTGGCTGG	481 TCAGCATGGCCCAGGATGGCCTGGACAGAGCACGTGTATGACCTCTTTGAGAAAGCCG 540	541 TGAAGGATTACATTTGTCCTAACATTTGGCTAGAGTATGGCCAGTACTCAGTTGGTGGGA 600	601 TTGGTCAGAAAGGTGGCCTTGAGAAAGTTCGCTCCGTGTTTGAAAGGGCTCTCTCGTCTG 660	661 TTGGTTTACATATGACCAAAGGACTCGCCCTCTGGGAGGCTTACCGAGAGTTTGAAAGTG 720	721 CGATTGTGGAAGCTGCTCGGCTTGAGAAAGTCCACAGTCTTTTCCGGCGACAGTTGGCGA 780	TCCCACTCTATGATATGGAGGCCACATTTGCAGAGTATGAAGAATGGTCAGAAGACCCCAA 	841 TACCAGAGTCAGTAATTCAGAACTATAACAAAGCACTACAGCAGCTGGAGAAATATAAAC 900 	901 CCTATGAAGAAGCACT	917	939 CTGGCAGAATATCAAGCATATATCGATTTTGAGATGAAAATTGGCGATCCTGCTCGCATT 998 1025 CTGGCAGAATATCAAGCATATATCGATTTTGAGATGAAATTGGCGATCCTGCTGCTT 1084	999 CAGTIGATCTTIGAGCGCGCCCTGGTCGAGAACTGCCTTGTCCCAGACTTATGGATCCGT 1058
qu	QQ	රු අ	Oy Op	oy G	à à	0 0 G	Qy Dp	Qy Pp	y a	Qy da	QV	QV Db	Qy	Qy	QQ QQ	oy da	oy da	Oy Dp
1692 TTTAGAAGATTGGGATATAGCTGTTCAGAAAACTGAAACCCGATTAGCTCGTGTCAATGA 1751	1745 GCAGAGAATGAAGGCTGCAGAAGGAAGCAGCCCTTGTGCAGCAAGAAGAAAAGGC 1804 	1805 TGAACAACGGAAAAGACCTCGGGCTGAGAAGGAAGCGTTAAAAAAGAAGAAAAA 1858 	RESULT 2 BC004547 15001 15001 UPC 12, THE 2001	ITION Homo sapiens, Similar to KIAA0156 gene product, clone . IMAGE:3958574, mRNA.	VERSION BC004547.1 GI:14709196 KEYWORDS HTC. SOURCE Homo sapiens. ORGANISM Homo sapiens		TITLE Direct Submission JOURNAL Submitted (14-MART-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	NSA REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov COMMENT Contact: MGC help desk Email: cgapbs-r@mail.nih.gov	Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural	<pre>sequencing center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@nhgri.nih.gov</pre>	Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Dietrich, N.L., Guan, X., Gupta, J., Ho, SL., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,	ricowell, J., realSul, K., Suyder, B., Stancripop, S., Thomas, P.J., Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, LH. and Green, E.D.	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 15 Row: d Column: 10 This clone was selected for full length sequencing because it	FEATURES This clone has the following problem: frame shifted. FEATURES 1. 1947	/db_xref="taxon:9606" /db_xref="taxon:9606" /clone="INAGE:958574" /lissue_type="Placenta, choriocarcinoma"	/lab_host="muc_val" /lab_host="blunghost="porp" /note="vector: porp" /note="vector: porp"	y Match 46.1%; Score 1752; DB 11; Length 1947; Local Similarity 95.3%; Pred. No. 0;	CONSCIVALIVE O; MISMATCHES IO; INDEES 82; ROGGGTCGGATGGCGACGGCCGAAACCTCGGCTTCAGAACCCCGAGGCTGA

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CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Sco
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lilsa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 42 Row: g Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7661951 This clone has the following problem: frame shifted.

Location/Qualifiers
Submitted (26-FEB-2002) National Institutes of Health, Mammalian
               Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
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ротв7"
567 г
                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                          Contact: MGC help desk
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                                                   TACAGTCAGTACCTAGATCGACAACTGAAAGTAAAGGATTTGGTTTTATCTGTACATAAC
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llarity 95.4%; Pred. No. 0;
Conservative 0; Mismatches
1. 1938
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 1938)
Strausberg, R.
Direct Submission

REFERENCE AUTHORS TITLE

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

BC024279 RESULT

1501 CTGCGTGATTATGCAGAACTGGGCTAGGATTGAGGCTCGACTGTGCAATAACATGCAGAA 1560 QY	OY 1664 CATGGAGACAGAAGGTTCTTTAGAAGATTGGGATATAGCTGTTCAGAAAACTGAAAC 1723 Db 1741 CATGGAGACAGAAGGTTCTTTAGAAGATTGGGATATAGCTGTTCAGAAAACTGAAAC 1800 QY 1724 CAGATTAGCTCGTCAATGAGAGAATGAGAGCAGAAGGAAG	RESULT 4 B0231651 B0231651 LOCUGS DEFINITION AGREWOORT_718202 NIH_MGC_92 Homo sapiens CDNA clone IMAGE.6066581 ACCESSION B0231651.1 G1:20413051 KEWWORDS BST. B0231651.1 G1:20413051 KEWWORDS BST. SOURCE ONGANISM Homo sapiens ENTARYOTA: Manmalia. Entheria: Primates; Catarrhini: Hominidae; Homo. Manmalia. Entheria: Primates; Catarrhini: Hominidae; Homo. AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE JOURNAL CONDECT: Extraoberg, Ph.D. CONDECT: Extraoberg, Ph.D. DNA Sequencia: Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencia by: Agrancia Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CONDA Library Preparation: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Http://image.lln.gov.ence.corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: LIAM1334 row: 1 column: 06 High quality sequence stop: 683. Alsource Augusters—"Homo sapiens" Alsource—"Angen: Ends: Math.MGC_92" (Clone_librany enriched for Clone_librany enriched for Average insert size 2.5 kb. Library enriched for Average insert size 2.5 kb. Library enriched for full length clones and constructed by Life Technologies.	BASE COUNT 231 a 235 c 255 g 151 t ORIGIN
	TTACATATGACCAAGGACTGGCCCTGGGAGGCTTACCGAGGTTTGAAAGGCGGTTTACATGACGAGGGTTTGAAAGGCGGGGGGGG	906 GAAGAAGCACT 911	1424 CTCCGTGATTATCCAGAACTGGCCTAGGATTGAGGCTCGACTGTGCAATAACATGCAGAA 1483

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                                                                                                     AGAAGAAATCTGTAAGGCTCATGGCACGTGAAGGACCTCAGGCTGGTCACCAACCGGGC
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                                                                                                                                      GCCGGACACGAAGCTCAGGCCACTCTTCGAGGCCTGTGGGGGAGGTGCTCCAGATCCGACC
                                                                                                                                                                      CATCTTCAGCAACCGTGGGGATTTCCGAGGTTACTGCTACGTGGAGTTTAAAGAAGAAGAA
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       Length 872;
       DB 14;
              .7e-170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 867.2;
Pred. No. 5.76
                       0; Mismatches
      22.8%;
99.7%;
             Best Local Similarity 99.7
Matches 869; Conservative
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                                                                      2042
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mRNA linear EST 24-MAY-2002 sapiens CDNA clone IMAGE:6014036

bp Homo

BQ430825 AGENCOURT_7769183 NIH_MGC_92 15', mRNA sequence. BQ430825.1 GI:21169901

> DEFINITION ACCESSION VERSION

RESULT 5 BQ430825

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122
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                               Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 CAGGAGGAAGGCGTGAGCGAGGGATGGGATGAGTACGCCATGGCTTCCTCCGCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 ACGCGTCCGATGGCGACTGCGGCCGAAACCTCGGCTTCAGAACCCGGAGGCTGAGTCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483 AGCATGGCCCAGGATGGCCTGGACAGAGCACGTGTATGACCTCTTTGAGAAAGCCGTG
                                                                                            Gene Collection (MGC)
                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13207 row. n column: 21
High quality sequence stop: 701.
                             Vertebrata; Eutel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14; Length 920;
                             Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.1%; Score 839.6; DB 14; 96.8%; Pred. No. 3.1e-164; ive 0; Mismatches 24;
                          Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 920)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 889; Conserv
human:
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725 720 785

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/db_xref="taxon:gaptens"
/db_xref="taxon:gaptens"
/clone="IMAGE:4762245"
/clone="IMAGE:4762245"
/clone="Lib="NiH_MGC_4762245"
/clone="Lib="NiH_MGC_476245"
/close="tayon:brain; vector:poTB7; site_1: XhoI; site_2: Anote="organ: brain; vector:poTB7; site_1: XhoI; site_2: Anote="tayon:brain; vector:poTB7; site_1: XhoI; site_2: BcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1:8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG682796 861 bp mRNA linear EST 01-MAY-2001
602651288F1 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:4762245 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I toasa; 1 to 80: 1 to 80: 1 to 80: 1 to 80: NIH-WGC http://mgc.nol.nih.gov/.
      541 GATTACATTTGTCCTAACATTTGGCTAGAGTATGGCCAGTACTCCAGTTGGTGGATTGGT
                                               786 CTCTATGATATGGAGGCCACATTTGCAGAGTATGAAGAATGGTCAGAAGAACCCAATACCA
                                                                                                                                                                                                                                                                                                                          GTGGAAGCTGCTCGGCTTGAGAAAGTCCACAGTCTTTTCCGGCGACAGTTGGCGATCCCA
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
ptlate: LLCMA615 row: p column: 22
High quality sequence stop: 856.
Location/Qualifiers
I. 861
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.2%; Score 805.6; 'DB 12; Length 861; 99.1%; Pred. No. 3.7e-157; ive 0; Mismatches 4; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                     846 GAG---TCAGTAATTCAGAACTATAACAAAGCACTACAGCAGCTG 887
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Matches 852; Conservative
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BG682796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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BG682796
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:5534381"
/clone=lib="MAGE:5534381"
/tissue_type="leiomyosarcoma"
/tish_host="DH10B (phage-resistant)"
/note="Cogan: uterus; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: Sali: cloned unidirectionally. Primer: Oligo dr. Average insert size 2.1 kb. "
191 c 289 g 182 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 897)
                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.m column: 06
High quality sequence stop: 744.
Location/Qualifiers
1. 897
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                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 810.6; DB 13; Length 897;
Pred. No. 3.4e-158;
); Mismatches 29; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Emall: cgapb.r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.3%;
Best Local Similarity 96.3%;
Matches 852; Conservative
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:5501938"
/clone=lib="NIH_MGC_67"
/tissue_type="retinoblastoma"
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/note="Organ: eye; Vector: PCMV-SPORT6; Site_1: NotI;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can Recount to I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM12139 row: e column: 11
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QY 2805 AACGGCCTG-CCGCGGCTCCTGCAGTTGCCGCCCCAGCAGCCACCGAGGCACCCAAGAT 2863	†	Db 664 AAATGCCTAACTTMACTCTGGCCGGCGGACCTCCCACCAGCAGTGCACTGGGGAT 605 Qy 2984 GGACAGGCCTGGTGTGCTGCGTGCTGCAACCACCAGTGGCTTAAACAGAA 3043	Db 604 GAACAGGCTGGTGTGCTGCGCGCTSGCAACCACAGATGGCTCTCGGCTTTAGACAGAA 545 OV 3044 AGGGAAGGGTTCTAAGTCAAGGCTTTCAGTGCTCCTCATATTGAGGGCAGTGGT 3103	5044 AGGGGAAGGGGTTCTAAGTCAAGACCTGTCAGGGCTCCCTCAATTGAGGGCAGTGGCA	QY 3104 GAAAAGTGACCACTCTGCAGGCTCGGGCCCAGGATGTGGTGTCCTGAGATAGTTTTGTATC 3163	OY 3164 TTAAAGACTGAGGCAAAGGGAAACGGGAACACACTGTTTTGAGACACAGTTGTCCA 3223 	OY 3224 AATGTTTCTGGCCAGCTCCGGCCCTTTTGTANGACACTTCTCTTCCACCCTGCACGC 3283	OY 3284 ACATGTGCCCGTCATTCTTTAATTTTAAAAGATGAAATGGCAGATGCTAGTAATTCACA 3343	Oy 3344 GAATGGCCTCTTGTGGGGGTGGGTTCTCAGGGAAGTCAGCTATAAAACATTTGCTGGAGTT 3403	Qy 3404 TIGITCAAIGGGCTGTGCAITTTATATATTATGTTTGTAAATGACATGTCAGCCCTTG 3463 	Oy 3464 TITCATGITICCIAAAAGCAGAATATITGCAACAITTGTTTGTATAGGAATTATTGG 3523 :	Oy 3524 CCACCTGCT-GTGGACTGTTTTCTTTGCCTAGTGACTAGTGACCTGTGTTGTCTAAACAT 3582	Oy 3583 GAGT 3586 Db 4 GAGT 1	RESULT 11 AU121811 LOCUS AU121811 LOCUS AU121811 AU121811 RAMMA1 Homo sapiens cDNa clone MAMMA1001023 5', mRNA sequence.	ACCESSION AU121811 VERSION AU121811.1 GI:10937046 KEYWORDS EST. SOHREE human	NISM	REFERENCE 1 (bases 1 to 843) AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
		QY 1438 AGAACTGGGCTAGGATTGAGGCTCGACTGTGCAATAACATGCAGAAAAGCTCGGGAACTCT 1497	OY 1498 GGGATAGCATCATGACCA-GAGGAAATGCCAACTACGCCAACATGTGGCTAGAGTATT 1554	1555 ACAACCTGGAAA 1566	Db 884 ACAACCCTGGAA 895 RESULT 10	AL5636187C LOCUS AL563618 844 bp mRNA linear EST 16-FEB-2001 DEFINITION AL563618 LTL NFL001 NBC4 Homo sapiens CDNA clone CSODD009YB08 3	ACCESSION AL563618 VERSION AL563618.1 GI:12913189 KEYWORDS EST. SOURCE hyman	_	ALTERACE I (DASSES I LO 844) AUTHORS LIWEB. Gruber, C., Jessee, J. and Polayes, D. TITLE Full-length cDNA libraries and normalization JUGNAL Unpublished (2001) COMMENT CONTACT: Genoscope	Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: sequeféquencascope.cns.fr, Web : www.genoscop	rce	/clone_lib="LTL_NFL001_NBC4" /sex="male"	/note="Organ: brain: Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6	VecCor. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com "	21	Best Local Similarity 95.7%; Pred. No. 1.5e-153; Matches 808; Conservative 19; Mismatches 15; Indels 2; Gaps 2;	Oy 2745 CAGCTGTCTACTGCCTGGTGCCCTGCAAGTGCTGCAGCTCCTCAGGCTGAG 2804

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/ Organism="homo sapiens"
/ Organism="homo sapiens"
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/ Clone="lib="taxon: 9606"
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E. 1 (bases 1 to 851)

I. Unpublished (1999)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Genomics, Inc.

Clone distribution: MgC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

Location/Oualitiers

Location/Oualitiers
                                                                                                                                                                                                                                                                                                                                                                                                        BI457408 851 bp mRNA linear EST 21-AUG-2001 603185548F1 NIH_MGC_42 Homo sapiens CDNA clone IMAGE:5258362 5',
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  GGTTTACATATGACCAAAGGACTCGCCCTCTGGGAGGCTTACCGAGAGTTTG-AAAGTGC
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96.7%; Pred. No. 9.4e-150;
iive 0; Mismatches 25;
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                                                                                                                                                                                                                                   Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
RESEARCH INSTITUTE; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
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                                                                                                                              Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
TTE1: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
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176 c 274 g 174 t
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/clone="MAMMA1001023"
/clone_lib="MAMMA1"
                         HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.hh.gov
Tissue Procurement: ATCC
                                      AAACCAGCTGGAGATTGAGAGACTGGAGGAGCAGTTGTCTATCAACGTCTATGACTACAA
                                                                                                     CTGCCATGTGGACTTGATCAGACT-GCTCAGGCTGGAAGGGGAGCTTACCAAGGTGAGGA
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/clone="IMAGE:634184"
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/tissue_type="neuroblastoma, cell line"
/tissue_type="neuroblastoma, cell line"
/tope="organ: brain, Vector: poTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCGAGGAGG]. Size=selected >500bp for average
insert size 1: 8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MCC Library."
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               Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortlum/LLNL at: http://image.llnl.gov.http://image.llnl.gov.plate: LLCM2540 row: i column: 13 Plate: LLCM2540 row: i column: 13 High quality sequence stop: 660.

Location/Qualifiers
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; Pred. No. 2.9e-149;
.0; Mismatches 34;
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Best Local Similarity 95.5%;
Matches 812; Conservative
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Oy 2697 CCCATGCTTTTGCCGCAGACCTAGGGGGAAGGGAAGGGA	2977 TTTGCCAAGCTGTTTCTGAGAAAGTGAACGGAGGCACCCAAGATGTCCAATGCCGAT 2877 TTTGCCAAGCTGTTTCTGAGAAAGTGAACGGGACGCTGGGAGCACCCAAGATGTCCAATGCCGAT 2877 TTTGCCAAGCTGTTTCTGAGAAAGTGAACGGGACGCTGGGAACAGGAAATGCCTTACTT 242 TTTGCCAAGCTGTTTCTGAGAAAGTGAACGGGACGCTGGGAACAGAAAGCCTTACTT 243 CAATTGCCAAGCTGTTTCTGAGAAAGTGAACGGGAACGAAC	2997 GTGCTGGCGGGGGGCCTCCCCCCAGCAGCGCGGGGGGGGG	3117 TCTGCAGGCTGGGCCCAGGATGTCTCTGAGATAGTTTTGTATCTTAAAGACTGAGG 3176	3297 ATTCTTTAAATTTTAAAAGATGAA-ATGGCAGATGCTAGTAATTCACAGAA-TGGCCTCT	OY 3471 TTTCTCAAAGATATTTGCAACATTTTGTTTTGTTTGTGTGGGGAATTATTGTGGGGGGGG	DEFINITION AU137933 789 bp mRNA linear EST 02-AUG-2002 DEFINITION AU137933 PLACE1 Homo sapiens cDNA clone PLACE1007533 5', mRNA Sequence. ACCESSION AU137933.1 GI:10999454 KEYWORDS EST. SOURCE human. ORGANISM Homo sapiens Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Qy 3143 GTCCTGAGATAGTTTGTATCTTAAAGACTGAGGCACAGAACGGAAACGAGAACACTG 3202 I	QY 3261 ACTTCTCTTCCACCCTGCACACGCACATGTGCCCGTCATTTTAAAAGATG 3318 DD 781 ACTTCTCTCCCACCTGCACAGGAACATGTGGCCCCGGTCAATTCTTTAAATTTT 840 QY 3319 AAATGCCAG 3328 DD 841 AAAAGAATGA 850		CREATUSE HOMO Saplens BURATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Jases 1 to 943) AUTHORS II-MGC http://mgc.nci.nih.gov/ TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M. A.G.E. CONSOTtium (LIMI.)	DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMI704 row* column: 21 High quality sequence stop: 741. FEATURES I. 943 //Organism="Homo sapiens" //db_xref="taxon:9606" //clone="Inparage"/ //clone=lib="NIH_MGC_48" //tissue_type="primary B-cells from tonsils (cell line)"	TINY 215	tch al Similari 864; Cons 637 AGCAACC 1

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                                                                                                      Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1512-3 Yana, Kisarazu, Chiba 292-0812, Japan
151-18 1-438-52-395
Fax: 81-438-52-396
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
              Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
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a 166 c 259 g 160
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/clone_lib="PLACE1"
                                                     human cDNA project
                                                               Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
 (bases 1 to 789)
                                        Isogai, T
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AAM40367 AAG39360 AAG52494 AAG52493 AAR52492 AAR43893 AAR43893 AAW00024 ABB28701

ABB58338 AAG39359 AAG39358

AAG48234

AAG48232 AAB92836 AAR79912 AAW84052 AAB48964

Smooth muscle myos Peptide #1352 enco Peptide #1389 enco Protein #1323 enco Human brain expres Human bone marrow Peptide #1349 enco

ABB33883 ABB19324 AAM54649 AAM67053 AAM14915

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ALIGNMENTS

RES	RESULT 1
AAY	AAY85422
Ωī	AAY85422 standard; Protein; 963 AA.
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AC	AAY85422;
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TO	23-JUN-2000 (first entry)
xx	
DE	Tumour antigen protein SART-3.
xx	
KW	Tumour antigen protein; SART-3; cytotoxic T-cell; HLA antige
XX	
so	Homo sapiens.
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Nd	WO200012701-A1.
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PD	09-MAR-2000.
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PF	27-AUG-1999; 99WO-JP04622.
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PR	28-AUG-1998; 98JP-0242660.
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PA	(SUMU) SUMITOMO PHARM CO LTD.
PA	(ITOH/) ITOH K.
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PI	Itoh K, Nakao M;
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DR	WPI; 2000-237868/20.
DR	N-PSDB; AAZ90783.
××	
PT	Tumor antigen protein SART-3 recognized by cytotoxic T-cells
PŢ	HLA antigen for treatment and diagnosis of tumors
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match Length DB

Score

Result Š.

1. SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2. SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:*
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cytotoxic T-cells binding tumors .

Tumour antigen pro Human SART3-IC-HER Human prostate can Peptide #2764 enco Peptide #2790 enco Protein #2727 enco Human brain expres Human bone marrow Peptide #2728 enco

AAY85422 AAE13123 AAB56918 ABB30113 ABB35284 ABB35284 AAM56114 AAM68486 AAM16294

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          This represents a tumour antigen protein (SART-3) which is recognized by cytotoxic T-cells binding to HLA antigen. SART-3 can be expressed by standard recombinant methodology. SART-3 and its peptide derivatives can be used in the prevention, treatment and diagnosis of tumours in vitro or in vivo.
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Claim 1; Page 54-58; 89pp; Japanese.
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Matches 963; Conserv
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                                                                                                                                                                                               Human SART3-IC-HER-2 membrane distal intracellular domain fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid molecules encoding such proteins. The IFPs comprise a polygeptide antique component and an immunostimulatory component derived from the intracellular domain of HER-2 protein which is effective to elicit a protective dendritic cell (DC)-induced T-cell mediated cellular immune response to the antigen. IFP or superactivated dendritic cells are used to treat cancer e.g. breast carcinoma, ovarian and colon cancer associated with a particularly antigen. The present sequence is a fusion protein which comprises human squamous cell carcinoma antigen, SART3-IC and mature human HER-2 membrane distal intracellular domain.
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of HER-2 and an antigen elicits an immune response to the antigen and
is useful for the treatment of associated cancer associated -
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                                                                                                                                                                                                                                                         Immunostimulatory fusion protein; IFP; antigen component; therapy; fimunuostimulatory component; T-cell mediated immune response; DC; dendritic cell; colon cancer; breast carcinoma; ovarian cancer; human; HER-2 membrane distal intracellular domain; SART3-IC;
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AAE13123 standard; Protein; 1179
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N-PSDB; AAD21574.
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Human; prostate cancer; prostate cancer antiyeu; uercorror, cordinatory; muscular; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antinifective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal; pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
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ISNPPQRKVPEKPETRKAPGGPMLLPQTYGARGKGRTQLSLLPRALQRPSAAAPQAENGP
                                                                                                                     EEKSALQALEMDRKSVEGRPMFVSPCVDKSKNPDFKVFRYSTSLEKHKLFISGLPFSCTK
                                                                                                                                                                                                                                                                              Peptide #2764 encoded by breast cell single exon nucleic acid probe.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences:
                                                                                                                                                                                                                                                                                                                                             1 MATAAETSASEPEAESKAGPKADGEEDEVKAARTRRKVLSRAVAAATYKTMGPAWDQQEE
than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                 probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                               Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GVSESDGDEYAMASSAESSPGEYEWEYDEEEEKNQLEIERLEEQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                             Score 526; DB 22;
Pred. No. 5.2e-34;
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                                                                                                                                                                                                                         10.5%; Sco.c.
100.0%; Pred. No. c...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0632366
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                                                                                                                                                                                                                                                                                             Matches 104; Conservative
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                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                               104 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
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03-AUG-2000
                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                         Best Local
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104 AA;

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                            9
                                                       probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays.
                                                                                                                                                                                                                               Protein #2727 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human hearts \boldsymbol{\cdot}
                                           1 MATAAETSASEPEAESKAGPKADGEEDEVKAARTRRKVLSRAVAAATYKTMGPAWDQQEE
                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.5%; Score 526; DB 22; Length 104; 100.0%; Pred. No. 5.2e-34; ive 0; Mismatches 0; Indels
 Length 104;
                                                                                                                                                                                                                                                    Human; gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                               61 GVSESDGDEYAMASSAESSPGEYEWEYDEEEEKNQLEIERLEEQ 104
                      Indels
10.5%; Score 526; DB 22;
100.0%; Pred. No. 5.2e-34;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; SEQ ID No 22498; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                                              ABB20728 standard; Protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0207456.
2000US-0608408.
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2000US-0234687.
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2000GB-0024263.
                                                                                                                                                                                                           (first entry)
                    104; Conservative
                                                                                                                                                                                                                                                                            congenital heart disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488899/53
           Similarity
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21-SEP-2000;
27-SEP-2000;
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30-JUN-2000;
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Query Match
           Best Loca
Matches
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Gaps

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10.5%, 100.0%; Pre-

Best Local Similarity 100. Matches 104; Conservative

Query Match

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MATAAETSASEPEAESKAGPKADGEEDEVKAARTRRKVLSRAVAAATYKTMGPAWDQQEE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe encoded protein SEQ ID NO: 28219.
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                         1 MATAAETSASEPEAESKAGPKADGEEDEVKAARTRRKVLSRAVAAATYKTMGPAWDQQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 28219; 650pp + Sequence Listing; English:
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                                                                                             61. GVSESDGDEYAMASSAESSPGEYEWEYDEEEEKNQLEIERLEEQ 104
                                                                                                                       61 GVSESDGDEYAMASSAESSPGEYEWEYDEEEEKNQLEIERLEEQ 104
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100.0%; Pred. No. 5.2e-34;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank
                                                                                                                                                                                                                                                                     AAM56114 standard; Protein; 104 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00667.
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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21-SEP-2000;
27-SEP-2000;
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us-09-763-985a-2.rag

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The present invention relates to human single exon nucleic acid probes (SENP: see AAIIO08-AAIIS459). The present sequence is a peptide encoded by one such probe. The SEMPS are derived from human HeLa cells. The SEMPs can be used to produce a single exon microarray, which can be used for massuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #2820 encoded by probe for measuring placental gene expression.
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Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.5%; Score 526; DB 22; Best Local Similarity 100.0%; Pred. No. 5.2e-34; Matches 104; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID No 21120; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
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                                                                                                                                                                                                                                                                                                                                                   (MOLE-), MOLECULAR DYNAMICS INC
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic disorder
               cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer
                                                                                        WO200157278-A2.
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27-SEP-2000;
04-OCT-2000;
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                                                                                                                           09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of single exon nucleic acid
                                                                                                                                                              Human bone marrow expressed probe encoded protein SEQ ID NO: 28792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO: 28792; 658pp + Sequence Listing; English.
                                                                                                                                                                                                  Human; bone marrow expressed exon; gene expression analysis; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GVSESDGDEYAMASSAESSPGEYEWEYDEEEEKNQLEIERLEEQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 526; DB 22;
Pred. No. 5.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5%; Scot.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                AAM68486 standard; Protein; 104 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00668
                                                                                                                       06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 AA;
                                                                                                                                                                                                                                                                                         WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2001
                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                    AAM68486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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AAM16294
ID AAM1
           RESULT 8
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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI40067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MATAAETSASEPEAESKAGPKADGEEDEVKAARTRRKVLSRAVAAATYKTMGPAWDQQEE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human peptide encoded by genome-derived single exon probe SEQ ID 27732
                                                                                                                                                         Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoldosis; pulmonary haemosiderosis; pulmonary histiccytosis; lymphangloleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; single exon probe; asthma; lung cancer; COPD; ILD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.5%; Score 526; DB 22;
100.0%; Pred. No. 5.2e-34;
iive 0; Mismatches 0;
                                                                                                                                                                                                                  Claim 27; SEQ ID No 12768; 322pp; English.
                                                                             DR;
                                                                             Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG38067 standard; Peptide; 104 AA.
                                      (MOLE-) MOLECULAR DYNAMICS INC.
                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-180312P.
26-MAY-2000; 2000US-207456P.
30-JUN-2000; 2000US-0608408.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hyaline membrane disease
                                                                             Hanzel DK,
                                                                                                                  WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 AA;
                                                                                                                                                                             in a human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200186003-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG38067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                             Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
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  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MATAAETSASEPEAESKAGPKADGEEDEVKAARTRRKVLSRAVAAATYKTMGPAWDQQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide #2710 encoded by probe for measuring breast gene expression.
                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5%; Score 526; DB 22; Length 104; 100.0%; Pred. No. 5.2e-34; .ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVSESDGDEYAMASSAESSPGEYEWEYDEEEEKNQLEIERLEEQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; SEQ ID No 29052; 654pp; English.
                                                                                                                                                                                                                                                                                           Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM04028 standard; Protein; 104 AA.
                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
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2000US-0234687.
2000US-0236359.
                                                                                         2000us-0180312.
2000us-0207456.
2000us-0608408.
2000us-0632366.
2000us-0234687.
2000us-0234887.
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2000US-0608408.
                                                     30-JAN-2001; 2001WO-US00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.59
Best Local Similarity 100.0
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human genetic disorders.
                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                         27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                    03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
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                                                                                                                                  30-JUN-2000
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                                                                                                                  26-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                           Penn SG,
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Gaps

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The control retained to a spatially-datesable set of single exon in clief acid probes for measuring single exon nuclet acid probes having one of for from human lung comprising single exon nuclet acid probes having one of for from human lung comprising single exon nuclet acid probes having one of complements or the 1287 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a collection of detectably labeled nucleic acids derived from human lung, comprising the novel set of muclet acid detectably labeled nucleic acids derived from human lung, comprising the array, identifying exons in a eukaryotic genome, comprising on mRNA, and (b) measuring the label detectably bound to each probe of the array, identifying exons in a eukaryotic genome, comprising complement identical to the predicted exon, the probe of the array, identifying exons in a eukaryotic genome, comprising comprising do adorithmical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon probe of the above mentioned microarray; assigning exons to a single exon probe of the above mentioned microarray; assigning exons to a single exon of above and (b) measuring the expression of each of the exons in the tissues and/or cell types using hybridisation to a single exon accordance and of the exons in the tissues and/or cell types indicates that expression analysis, and for identifying exons in a gene, particularly capped expression analysis, and for identifying exons in a gene, particularly diseases of the exons should be assigned to a single exon in a gene, particularly using human lung derived mRNA and for the study of lung diseases combinant and partern of a such as asthma, lung cancer, chronic obstructive pulmonary wispassion analysis, and for identifying exons in a gene, particularly assigned to a single exon probe of lung disease. (COPP), interstitial lung disease (ILD); familial idiopathic pulmona
                                                                                                                                                                                                                                                            Spatially-addressable \ set \ of \ single \ exon \ nucleic \ acid \ probes, \ used \ to \ measure \ gene \ expression \ in \ human \ lung \ samples \ -
                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID No 27732; 634pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                   Rank DR;
                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                 Chen W,
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-234687P.
27-SEP-2000; 2000US-23659P.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      directly from WIPO at
                                                                                                                                                                 Penn SG, Hanzel DK,
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104 AA; Sequence

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                                                              MATAAETSASEPEAESKAGPKADGEEDEVKAARTRRKVLSRAVAAATYKTMGPAWDQQEE
                                 Gaps
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0
10.5%; Score 526; DB 23; Length 104; 100.0%; Pred. No. 5.2e-34; ive 0; Mismatches 0; Indels (
                               104; Conservative
                Similarity
 Query Match
Best Local 9
                              Matches
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GVSESDGDEYAMASSAESSPGEYEWEYDEEEEKNQLEIERLEEQ 104 61

RESULT 13 . .

Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; dimmune modulation; haematopolesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; cardiovascular disease; immune system disorder; organ transplantation; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide. Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ Human ORF2630 protein, SEQ ID NO:5260 ABP33657 standard; Protein; 108 AA. 24-MAY-2001; 2001WO-US17076. 24-MAY-2000; 2000US-206690P. 08-JUL-2002 (first entry) Leach MD, Shimkets RA; (CURA-) CURAGEN CORP. WPI; 2002-106200/14. N-PSDB; ABN77683 transplantation WO200190366-A2. Homo sapiens. 29-NOV-2001. ABP33657; ABP33657

Claim 10; Page 1566-1567; 2508pp; English.

Geguences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-8AN75054 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polymucleotides at least 85% identical to referred to as ORFX) proteins, polymucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polymucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of acreening for modulators of ORFX expression or polypeptides, methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haematopolesis requirity, chemotactic/ chemokinetic activity, haemostatic activity, thrombolytic activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, the content of acids and antibodies may be used in the treatment of cancers, the content of the contents. ester neurological disorders such as epilepsy and Alzheimer's disease, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol est storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a proliferative disorders such as psoriasis and benign tumours, other

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Gaps

246

288

343 372 433

493 542 599 602 658 662

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| | : | : : | : | | : | | 373 DVLWLSYIEFIQFEGVTVPENEDENEVTAEMVAKRAKRLGKGFLRNTELDLANRGVRSHP 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  663 AAGPAGKCAAVDVEPPSKQKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSMQEPDTKL 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                723 RPLFEACGEVVQIRPIFSNRGDFRGYCYVEFKEEKSALQALEMDRKSVEGRPMFVSPCVD 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSDDEPSVEETEGGNAAGR-----GRARNDSSSSSDDVGVIE--GSELESNSEVSSDSD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELTKVRMARQKMSEIFPLTEELWLEWLHDEISMAQDGLDREHVYDLFEKAVKDYICPNIW 186
                                                                                                                                                                                                                                                                                                                                                                                                 SD----SDNAGGGNQLERSY---QELNALPSKKFAQMVS-----LIGIAFKLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 VHSLFRRQLAIPLYDMEATFAEYEE-----WS----EDPIPESVIQNYNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: | :: | :: | :: | DYDVERPDFGDKLRSLISTITDENEAAAFVEMLQKHCVTWTCNVEQRQMIKSVVDKFKQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQQLEKYKPYEEALLQAEAPRLAEYQAYI-DFE-MKIGDP---ARIQLIFERALVENCLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDETTRGWDWSE-----QHKAHYYDVETLSLDDDLKNAVIRFIFERSVAKFPIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the detection of ORFX genomic sequences
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source of primers and probes, in the detection of ORFX genomic sequenc or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX protein, and also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                            Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
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90.3%; Pred. No. 1.3e-25;
tive 1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; SEQ ID 5934; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GVSESDGDEYAMASSAESSPGEYEWEYDEEEEK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GVSESXGDEYAMASSAESSPGEYEWNWTKRRK 93
                                                                                                                                                                                                                                                                                                         Human secreted protein, SEQ ID NO: 5934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duclert A,
                                                                                                                                                                                             AAG01853 standard; Protein; 100 AA.
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Matches 84; Conservative
                                                                                         930 SNDDFRKLFLK 940
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N-PSDB; AAC01859.
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                                                                                                                                                                                                                                                                                                                                                                                                                                EP1033401-A2
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Search completed: June 18, 2003, 13:50:25 Job time : 46 secs Appli Appli Appli Appli Appli

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TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
TITLE OF INVENTION: APPLICATIONS
NUMBER OF SEQUENCES: 10
OORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            554 RTEGSLEDWDIAVQKTETRLARVNEQRMKAAEKEAALVQQEEEKAEQRKRAR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/N7/25/7
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5.4%; Score 272; DB 1;
Best Local Similarity 22.2%; Pred. No. 5.5e-13;
Matches 84; Conservative 84; Mismatches 172;
US-08-195-487-4
US-08-483-924-4
US-09-452-294-1
US-08-973-273-26
US-08-973-273-3
US-08-990-114-1
US-08-990-114-1
US-08-929-329-5
US-09-929-329-5
US-09-929-329-5
US-08-929-329-5
US-08-928-33-4
US-08-928-33-4
US-08-928-33-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Weiser & Associates
STREET: 230 S. Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                     PCT-US95-16216-1
                                                                                                                                                                                                                                                                                                                                        US-07-881-075-2
US-08-120-827-2
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CLASSIECATION: 435
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NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFRENCE/CDOCKET NUMBER: 377.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICANT: Kondo, Keiji
APPLICANT: Inouye, Masayori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 4:
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Sequence 4, App
Sequence 1, App
Sequence 183, A
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Sequence 4,
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Sequence 3,
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-478-675-3
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US-08-467-781-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                                        protein search, using sw model
                                                                                                                                               June 18, 2003, 13:49:38
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Result ٠ اي 169.5 169.5 169.5 168.5 168.5 166.5

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Sequence:

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Run on:

Scoring table:

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Minimum DB Maximum DB

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                                                                                                                                                                     240 NCDMSTSKPAGNNDRAKKFGDTPSEPSDTLFLGNLSFNADRDAIFELFAKHGEVVSVRIP 299
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            --AEKKALKKKKKIRGPEKRGADEDDEKEWGDDEEEQPSKRRVENSIPAAGET 657
                                                                              QNVEVAAGPAGKCAAVDVEPPSKQKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSMQE 717
                                                                                                                                                                                                                 776 FVSPCVDK--SKNPDFKVFRYSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLV 833
                                                                                                                                                                                                                                                                                                           APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN NUCLEOLIN-LIKE PROTEIN
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,114
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0451 US
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Sequence 3, Application US/08990114
Patent No. 5932475
                                                                                                                                                                                                                                                                                                                                                                               893 PGGPMLLPQTYGARGKGR 910
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REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 714 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --KRDMPKVLHDSSK--DSITVFVSNLPYSMQEPDTKLRPLFEACGEVVQ 734
                                                                                                                                                                                                                                                                                                                                                                                                   735 IRPIFSNRGDFRGYCYVEFKEEKSALQALEMDR-KSVEGRPMFVSPCVDKSKNPDFKVFR 793
                                                                            583 AAEKEAALVQQEEEKAEQRKRARAE------KKALKKKKIRGPEKRGADEDDE
                                                                                                                 187 ASEDEDEEEEEEEEEEEDBEEEEEDDSEEEEAMEITPAKGKKAPAKVVPVKAKNVAEEDDDDE
                                                                                                                                                                                              247 EEDEDEEEDEEEEEEEEEEEEEEEEEEEEFPVKPAPGKRKKEMTKOKEVPEA-KKOKVEGSEST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               794 YSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTNRAGKPKGLAYVEYENESQ
                                                                                                                                                           ---PSKRRR---VENSIPAAGETQNVE----
                                       105;
Length 714;
                                       Indels
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APPLICANT: Bandman, Olga
APPLICANT: Vue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN NUCLEOLIN-LIKE PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                       67; Mismatches 134;
  DB 2;
                  8e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
  4.5%; Score 224.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Incyte Pharmaceuticals, Inc.
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Patent No. 6313266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET UMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
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                                     Conservative
                                                                                                                                                           631 KEWGDDEEEQ-----
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                  Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                    e87 SL-----
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  Query Match
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617 IRGPEKRGADEDDEKEWGDDEEEQPSKRRRVENSIPAAGE--TQNVEVAAGPAGKCAAVD 674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 QAPGNPVLAVQI-----NQDKNFAFLEFRSVDETTQAMAFDGIIFQGQSLKIRRPHDY 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    778 SPCVDKSKNPDFKVFRYSTSL---EKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVT 834
                                                                                                                                                                                                                                                                                                                                                                                          559 LEDWD-IAVQKTETRLARVNEQRMKAAEKEAALVQQEEEKAEQR-KRAREKKALKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    727 EACGE---VVQIRPIFSNRGDFRGYCYVEFKEEKSALQALEMDRKSVEG-----RPMFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 QPLPGMSENPSVYVPGVVSTVVPDSAHKLFIGGLPNYLNDDQVKELLTSFGPLKAFNLVK
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APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL HUMAN NUCLEIC ACID BINDING PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                             Length 475;
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                 68; Mismatches 174;
                                                                                                                                                                                                                                                                                                           4.1%; Score 204; DB 2; 22.9%; Pred. No. 1.2e-07;
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SOCTWARE: FASTSEÖ VERSION 1.5
SOCTWRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09195855
Patent No. 6015788
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
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                                                                                                         LENGTH: 475 amino acids
                                          TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 22.99
Matches 85; Conservative
                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 267188
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352 NQTPVTLQVPG 362
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                                                                                                                          TYPE: amino acid STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                     US-08-698-407-4
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US-09-195-855-4
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                                                                                                                                                                                                                                                                                                                                                                  631 KEWGDDEEEQ----- 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 ELTGLKVFGNEIKLEKPKG-RDSKKVRAARTLLAKNLSFNITEDE--LKEVFE---DALE 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               735 IRPIFSNRGDFRGYCYVEFKEEKSALQALEMDR-KSVEGRPMFVSPCVDKSKNPDFKVFR 793
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                                                                                                                                                                                                                                                  Gaps
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APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Jannice
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hillman, Jennifer L.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: HILLMAN, Jennifer L.
CORRESPONDENCE S. 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---VAAGPAGK--CAAVDVEPPSKQK-----
                                                                                                                                                                                                      Length 714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 AKEALNSCNKMEIEGRTIRLELQGP----RGSPNARSQP 570
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                                                                                                                                                                                                      4.5%; Score 224.5; DB 4;
23.5%; Pred. No. 5.8e-09;
tive 67; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 Porter Drive CITY: Palo Alto
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APPLICATION NUMBER: US/08/698,407
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    583 AAEKEAALVQQEEEKAEQRKRARAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSTEM: DOS
FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
                       LENGTH: 714 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                              Query Match
Best Local Similarity 23.58
Matches 94; Conservative
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SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Diskett
                                                                                TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: GenBank CLONE: 128842
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US-08-698-407-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1123 -MRRDLEEATLQHEATAAALRKKHADSVAELGEQIDNLQRVKQKLEKEKSEFKLELDDVT 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 GQYSVGGIGQKGGLEKVRSVFERALSSVGLHMTKGLALWEAYREFESAIVEAARLEKVHS 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 PYEEALLQAEA-----GPRLAEYQAYIDFEMKI---------GDPARIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 LIFERALVENCLVPDLW-----IRYSQYLD----RQL----KVKDLVLSVHNRAIRNCPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 SKAGPKADGEEDEVKAARTRRKVLSRAVAAATYKTMGPAWDQQEEGVSESDGDEYAMASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 AESSPGEYEWEYDEEEEKNQLEIE-----RLEEQLSINVYDYNCHVDLIRLLRLEGELTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 VRMARQKMSEI-FPLTEELWLEWLHDEISMAQDGLDREHVYDLFEKAVKDYICPNIWLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 TVALWSRYLLAMERHGVDHQVISVTFEKALNAGFIQATDYVEIWQAYLDYLRRRVDFKQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 SSKELEELRAAFTRALEYLKQEVEERFNESGDPSCVIMQNWARIEARLCNNMQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KREAEFQK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----EEISERLEEA
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                       COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.1%; Score 202.5; DB 4 Best Local Similarity 19.6%; Pred. No. 1.2e-06; Matches 195; Conservative 154; Mismatches 342
                                                                                                             APPLICATION NUMBER: US/08/938,105 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1291 --LLREQYEEEMEAKAELQRVLS---
                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: CTOOK, Wannell M.
REGISTRATION NUMBER: 31,071
REFRENCE/DOCKET NUMBER: 3595
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                           TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1886 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1074 ERTARAKVEKLRSDLTREL
      Floppy disk
                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-938-105-3
                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 QAPGNPVLAVQI-----NODKNFAFLEFRSVDETTQAMAFDGIIFQGQSLKIRRPHDY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEPPSKQKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSMQE------PDTKLRPLF 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 QPLPGMSENPSVYVPGVVSTVVPDSAHKLFIGGLPNYLNDDQVKELLTSFGPLKAFNLVK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSDFDEFEROLNENKQERDKENRHRKRSHSRSRSRDRKRRSRSRDRRNRDQRSASRDRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 617 IRGPEKRGADEDDEKEWGDDEEEQPSKRRRVENSIPAAGE--TQNVEVAAGPAGKCAAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EACGE----VVQIRPIFSNRGDFRGYCYVEFKEEKSALQALEMDRKSVEG-----RPMFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPCVDKSKNPDFKVFRYSTSL - - - EKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRA-GKPKGLAYVEYENESQASQAVMKMDGMTIKENIIKV------AISNPPQRKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        559 LEDWD-IAVQKTETRLARVNEQRWKAAEKEAALVQQEEEKAEQR-KRARAEKKALKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
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US-08-938-105-3
Sequence 3, Application US/08938105
Fatent No. 6353151
GENERAL INFORMATION:
APPLICANT: Leliwand, Leslie A.
TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
SCORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.1%; Score 204; DB 3;
Best Local Similarity 22.9%; Pred. No. 1.2e-07;
                                                                            ATTORNEY CATE.

ATTORNEY ACTENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0116 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/698,407
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
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                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 80203
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US-09-195-855-4
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Sequence 1, Application US/08120827

Sequence 1, Application US/08120827

Patent No. 5525495

GENERAL INFORMATION:
APPLICANT: KENE, JACK D.
APPLICANT: KING, PETER H.
APPLICANT: LEVINE, TODD
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
NUMBER OF SEQUENCES: 101
  284 NAGNDTQTKGVGFIRFDKREEATRAIIALNGTTPSSCTDPIVVKFSNTPGSTSKIIQPQL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                     835 NRAG--KPKGLAYVEYENESQASQAVMKMDGMTIKE--NIIKVAISNPP-----QRKV 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 PAFLINPQLVRRIGGAMHTPV----NKGLARFSPMAGDMLDVMLPNGLGAAAAATTLAS 398
                                                                                                                                                               675 VEPPSKQKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSMQEPDTKLRPLFEACGEVVQ 734
                                                                                                                                                                                                                                                                                                                                                        775 MFVSPCVDKSKNPDFKVFRYSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVT 834
                                                                                                                                                                                                                                                                                          238 SFARPSSDAIKGAN------LYVSGLPKTWTQQELEAIFAPFGAIITSRILQ
                                                                       KKIRGPEKRGADEDDEKEWGDDEEEQPSKRRRVENSIPAAGETQNVEVAAGPAGKCAAVD
                                                                                                                                                                                                                                                             735 IR-----LEMDRKSVEGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PE--KPETRKAPGGPMLLPQTYGARGKGRTQLS-------LLPRALQRPSAAAPQAEN
                                                                                                                 -----GSNG-----GSNG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: P.C.
1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/120,827
FILING DATE: 15-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 714-158-0 CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPAAAPAV----AAPAATEA 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 GPGGAYPIFIYNLAPETEEA 418
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NAME: Oblon, No. 5525495man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703)413-3000
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS: ADDRESSE: OBLON, SE
                                                                                                                   124 POOAOPNTNG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             16;
1496 AEASLEHEEGKILRAQLEFNQIKAEI---ERKLAEKDEEMEQAKRNHLRVVDSLQTSLDA 1552
                                                                                                                                                                                                                                                                                 .654 ELIETSERVOLLHSQNTSL-----INOKKKMDADLSQLQTEVEEAVQECRNAEEK 1703
                                                                                      553 ETRSRNEALRVKKKM--EGDLNEMEIQLSQANRIAS---EAQKHLKNAQAHLKDTQLQLD 1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       564 IAVQKTETRLA-----RVNEQRMKAAEKEAALVQQEEEKAEQRKRARAEKKALKKK 614
                                                                                                                                       ----LHDSSKDSITVFVSNLPYSMQEPDTKLRPLFEACGEVVQIRPIFSNRGDFRGYCYV 751
                                                                                                                                                                                                                                                                                                                             801 HKLFISGLPFSCTKEELEEICKAH------GTVKDLRLVTNRA-----GKPKGLAY 845
                                              EEEQPSKRRRVENSIPAAGETQNVEVAAGPAGKCAAVDVEPPSKQKEKAASLKRDMPKV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 140; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                  752 EFKEEKSALQALEMDRKSVEGRPMFVSPCVDKSKNPDFKVFRYSTSL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.0%; Score 201; DB 1; L 20.7%; Pred. No. 2.1e-07; Live 73; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          846 V----EYENESQASQA--VMKMDGMTIKENIIK 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5444149man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 714-154-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/881,075
FILING DATE: 19920511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07881075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: KEENE, JACK D.
APPLICANT: KING, PETER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 20.78
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248855 OPAT UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-07-881-075-1
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CLASSIFICATION:
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Sequence 4, Application US/09104324B Patent No. 6232460 GENERAL INFORMATION:
                  NAME: Oblon, No. 5773246man F. REGISTRATION NUMBER: 24,618
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                                      24,618
   ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-478-675-1
                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                       16;
                                                                                                                                                                      64 ΙΩΝΌΩΩΩΤΩΩΑΝΑΑΑΑΑΝΤΩΩΙΩΩΩΩΩΑΝΝΑΩΩΑΥΝΌΩΩΩΩΑΑΝΥΩΩΑΑΝΟΩΩΑΝΥΡΩ 123
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                                                                                                         Gaps
                                                               Query Match
4.0%; Score 201; DB 1; Length 485;
Best Local Similarity 20.7%; Pred. No. 2.1e-07;
Matches 91; Conservative 73; Mismatches 136; Indels 140;
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
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PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/120,827
FILING DATE: 15-SEP-1993
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COMPUTER: IBM PC compatible
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APPLICANT: KEENE, JACK D.
APPLICANT: KING, PETER H.
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   ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-120-827-1
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COUNTRY: U.S A
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TOPOLOGY:
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Ozlem; Sahin, Ugur; Pfreundschuh, Michael
Methods For Diagnosis And Treating Cancers,
And Methods For Identifying Pathogenic Markers In A Sample
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                               4.0%; Score 201; DB 1; 1
20.7%; Pred. No. 2.1e-07;
tive 73; Mismatches 136;
REFERENCE/DOCKET NUMBER: 714-158-0 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-2300
TELEFAX: (703)413-220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acid
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1082 LKKK------GFDINQQNSKIEDEQALALQLQKKLKEN------QARIEELEEELEA 1126
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        673 VDVEPPSK----QKEKAASLKRDMPKVLHDSSKDSIT-VFVSNLPYSMQEPDTKLRPLFE 727
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                                                                                 ACGEVVQIRPIFSNRGDFRGYCYVEFKEEKSALQALEMDRKSVEGRPMFVSPCVDKSKNP
                                                                                                                      --SQTVS----PKAYTVKTP
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                                           769 IEREEKEKLKREAKENTATLK-----EKKDKKTQTFLLETPEIYWKLDSKAVP-
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APPLICANT: Benichou, Gilles
APPLICANT: Fedoseyeva, Eugenia
TITLE OF INVENTION: Involvement of Autoantigens in Cardiac
TITLE OF INVENTION: Graft Rejection
FILE REFERENCE: UCSF-090
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19.6%; Pred. No. 2.6e-05;
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Best Local Similarity 19.6%; Pred. No. 2.6e-
Matches 190; Conservative 148; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: UCSF-090
CURRENT APPLICATION NUMBER: US/09/310,187A
CURRENT FILING DATE: 1999-05-12
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944 KFGAIRKMR 952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       610 NKNKYIE------ELQQENKALKKKGTAESKQLNVYEIKVNKLELELESAKQKFGEI 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 SPGEYEWEYDEEEEKNOLEIERLEEQLSINVYDYNCHVDLIRLLRLEGELTKVRMARQKM 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 SEIFPLTEELWLEWLHDEISMAQD--GLDREHVYDLFEK---AVKDYICPNIWLEYGQYS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 ----EFESAI-----VEAARLEKVHSLFRRQLAIPLYDMEATFAEYEEWSEDPIPES 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 FVVTEFETTVCSLEELLRTEQORLEKNED----QLKILTMELQKKSSELEEMTK----- 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 VIQNYNKALQQLEKYKPYEEALL--QAEAPRLAEYQAYIDFEMKIGDPARIQLIFERALV 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 ENCLVPDLWIRYS-----QYLDRQLKVKDLVLSVHNRAIRNCPWTVALWSRYLLAMERH 392
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|LEYVREELKQKRDE-------VKCKLDKSEENCNNLKK------QVE
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 EVKAARTRRKVLSRAVAAATYKTMGPAWDQQE-----
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,324B
FILING DATE: 25-June-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGGIGQKGGLEKVRSVFERALSS----
                                                                                                                                                                                                    LUD 5491
                                                                                                                                                       NAME: Hanson, No. 6232460man D. REGISTRATION NUMBER: 30,946
                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,702
FILING DATE: 15-JOLY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 976 amino acids
TYPE: amino acid
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US-09-104-324B-4
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APPLICANT: Kondo, Keiji.
APPLICANT: Inouye, Masayori
TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
TITLE OF INVENTION: APPLICATIONS
    -- FEACGEVVQIRPIFSNRGDFR 746
                                                                                                                                                                              -KRDMPKVLHDSSKDSITVFVS 709
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                          801 HKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTNRAGKPKGLAYVEYENESQASQAVMK
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                                                                                                                                                                                                                                                          MDGMTIKENIIKVAISNPPQRKVPEKPETRKAPGGPMLLPQTY 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.4e-06;
  692 MPKV-LHDSSKDSITVFVSNLPYSMQEPDTKLRPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: Weiser & Associates
: 230 S. Fifteenth Street, Suite 500
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.6%; Score 178.5; Best Local Similarity 26.1%; Pred. No. 6.4e Matches 61; Conservative 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          660 VEVAAGPAGKCAAVDVEPPSKQKEKAASL-
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FILING DATE: 11-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/07667276A Patent No. 5470971 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: ""."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 11 CLASSIFICATION:
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COUNTRY:
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CITY: P}
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                                                                                                                                                                              1674 AIV------ERRNNLLQA--ELEELRAVVEQTERSRKLAEQELIETSERVOLLH 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1780 HLERMKKNMEQTIKDLQHRLDEAEQIALKGGKKQLQKLEARVRELEGELEAEQKRNAESV 1839
                                    1344 LLREQYEEFTEAKAELQRVLSKANSEVAQW------RTKYETDAIQRTEELEEAKKK 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1720 SQNTSLINQKKKMESDLTQLQSEVEEAVQECRNAEEKAKAITDAAMMAEELKKEQDTSA
---HQVISVTFEKA-LNAGFIQATDYVEIWQAYLDYLRRRVDFKQDSSKELEELRAAFTR
                                                                                                                                                                                                                                TEGSLED--WDIAVQ-----KTETRLARVNEQ-RMKAAEKEAALVQQEEE-KAEQRKRAR
                                                                                                                                                                                                                                                                                                              ---- DDEEEQPSKRRVENS
                                                                                                                                                                                                                                                                                                                                                                                  651 IPPAAGETQNVEVAAGPAGKCAAVDVEPPSKQKEKAASLKRDMPKVL-----HDSSKDSI
                                                                                                                                                                                                                                                                                                                                                                                                              LWDSIMTRGNAKYANMWLEYYNLERAHGDTQHCRKALHRAVQCTSDYPEHVCEVLLTMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                              705 TVFVSNLPYSMQEPDTKLRPLFEACGEVVQIRPIFSNRGDFRGYCYVEFKEEKSALQALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475c1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FEASLED for Windows Version 3.0
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23.3%; Pred. No. 2.9e-06;
ive 51; Mismatches 104; Indels
                                                                          ALEYLKQEVEERFNESGDPSCVIMQNWARIEARLCNNMQ---;---
                                                                                                                                                                                                                                                                                                          AEKKALKKKKIRGPEKRGADEDDEKEWG-----
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Patent No. 6444425
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1840 KGMRKSERRIK 1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.6
Best Local Similarity 23.3
Matches 66; Conservative
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LENGTH: 255
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us-09-763-985a-2.rai

OY 848 YENESOASOAVMKMDGMTIKENIIKVALSNPPORKVPEKPETRKAPGGPMLLPOTYGARG 907 :: : : :	1911 15 191	Db 148 GQSLGYGFVXYYKQEDAEKAINALNGLRLQNKTIKVSIARPS
145 EIDGRSISLYYTGEKKGONSKTLVLSNLSYSATEETLQEVFEKA 188 QY 825 GTVKDLRLVTNRAGKPKGLAYVEYENESQASQAVMKMDGMTIKENIIKVAISNP 878	PREBUT 14 105-07-881-075-3 105-07-881-075-3 105-07-881-075-3 105-07-881-075-3 105-07-881-075-3 105-07-881-075-3 105-07-881-075-3 105-07-08-07-075-3 105-07-08-07-075-3 105-07-08-07-07-07-07-07-07-07-07-07-07-07-07-07-	OY 794 YSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTNRAGKPKGLAYVE 847

us-09-763-985a-2.rai

0y	848 YENES	848 YENESQASQAVMKMDGMTIKENIIKVAISNPPQRKVPEKPETRKAPGGPMLLPQTYGARG 907
qq	:: 249 FDQRF	13
ογ	908 KGRIQ	908 KGRTQLSLLPRALQRPSAAAPQAENGPAAAPAVAAPAATEAPKMSNA 954
QQ	288	288SMQPLAAYIAPQNTRGGRAFPANAAAGAAAAAAAIHPNA 328
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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 18, 2003, 13:51:48; Search time 55 Seconds Run on:

(without alignments)
1894.603 Million cell updates/sec

1 MATAAETSASEPEAESKAGP........AATEAPKMSNADFAKLFLRK 963, US-09-763-985A-2 4994 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

417779 seqs, 108206813 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Potal number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score 4989 2918 526 231 225 224:5	Query Match 199.9 10.5 4.6 4.5	Suery Match Length DB 1179 10 19.9 1179 10 10.5 104 10 4.6 687 9 4.5 714 10	DB 10 10 10 10 10 10 10 10 10 10 10 10 10	US-09-821-883-29 US-09-925-300-1496 US-09-964-761-36026 US-09-969-384-27 US-09-925-301-1012	Description Sequence 29, Appl Sequence 1496, Ap Sequence 27, Appl Sequence 27, Appl Sequence 37, Appl
7 10 11 11 11 12 14 15 16 17 18	217 208.5 208.5 208.5 208.5 206.5 199.5 199.5 198.5 188.5	444444444mmmm 	11945 11945 11945 11945 11945 11945 11945 11203 1203 1488	10 10 10 10 10 10 10	US-09-864-761-34622 US-10-171-311-164 US-09-927-597-2 US-09-927-597-4 US-09-927-597-4 US-09-927-597-4 US-09-833-790-234 US-09-752-639-153 US-09-969-188-153 US-09-925-300-1554 US-10-153-668-320 US-10-153-668-320	Sequence 34622, A Sequence 164, App Sequence 2, Appli Sequence 162, Appli Sequence 234, Appli Sequence 153, App Sequence 153, App Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 320, App Sequence 320, Appl Sequence 43, Appl Sequence 432, Appl Appl Sequence 432, Appl Appl Sequence 432, Appl Appl Appl Appl Appl Appl Appl App

777	Sequence 5, Appl. Sequence 5, Appl. Sequence 128, Appl. Sequence 10, Appl. Sequence 27, Appl. Sequence 388, Appl.	392, 272, 4611, 16, 7	16, 16, 16, 16,	нана
US-10-146-473-41 US-10-082-830-260 US-09-854-133-183 US-09-738-973-183	US-0 US-0 US-0 US-1 US-1		US-10-140-470-16 US-10-175-746-16 US-10-176-918-16 US-10-176-921-16 US-10-137-865-16 US-10-140-474-16	
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22 23 23 23	25 25 26 28 29	30 30 30 30 30 30 30 30 30 30 30 30 30 3	337 337 440 41	4 4 4 4 2 6 4 6

ALIGNMENTS

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181 ICPNIWLEYGQYSVGGIGQKGGLEKVRSVFERALSSVGLHMTKGLALWEAYREFESAIVE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GVSESDGDEYAMASSAESSPGEYEWEYDEEEEKNQLEIERLEEQLSINVYDYNCHVDLIR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1179;
                                                                                                                                                                      TITLE OF INVENTION: Compositions and Methods for Dendritic TITLE OF INVENTION: Compositions and Methods for Dendritic TITLE OF INVENTION: Coll-based Immunotherapy FILE REFERENCE: 7636-0022.30
CURRENT APPLICATION NUMBER: US/09/821,883
CURRENT FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: EastSEQ for Windows Version 4.0
LENGTH: 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                        Sequence 29, Application US/09821883; Patent No. US20020061310A1; GENERAL INFONATION:
APPLICANT: Laus, Reiner
APPLICANT: Vidovic, Damir
APPLICANT: Graddis, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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RESULT 1
US-09-821-883-29
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                  DESPTPVTFEKALNAGFIQATDYVEIWQAYLDYLRRRVDFKQDSSKELEELRAAFTRALE
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                                            Score 2918; DB 10;
Pred. No. 7.3e-178;
0; Mismatches 5;
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-366
PRIOR PLICATION NUMBER: US 99/632,366
PRIOR PLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36026, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
                                             Query Match 58.4%;
Best Local Similarity 99.1%;
Matches 564; Conservative
sapiens
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EFERVRVIYKY--ALDRISKQDAQE------LFKNYTIFEKKFGDRRGIEDIIV 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AR---QKMSEIFPLTEELWLEWLHDEISMAQDGLDREHVYDLFEKAVKDYICPN-IWLEY 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TYMEEMLGNVAG---ARQVFER-----WMEWQPEEQAWHSYINFELRYKEVDRARTIYE 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379 -VALWSRYLLAMERHGVD----HQVISVTFEKALNAGFIQATDYV----EIWQAYLDYL 428
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                                                                                                                                                                                                                                                                                                                                                                                                                               282; Indels 184;
                                                                                                                                                                                                                                                                                                                                                                           4.6%; Score 231; DB 9; Length 687; 21.2%; Pred. No. 1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
     APPLICATION NUMBER: PCT/US01/10542
PRIOR APPLICATION NUMBER: PCT/US01/1054
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
PRIOR RILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.6%; Sco
Best Local Similarity 21.2%; Pro
Matches 155; Conservative 110;
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US-09-969-384-27
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US-09-925-301-1012
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LENGTH: 687
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TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PT055P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MATAAETSASEPEAESKAGPKADGEEDEVKAARTRRKVLSRAVAAATYKTMGPAWDQQEE
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 3.8

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 3.4

OTHER INFORMATION: SYPRESSED IN HELLO, SIGNAL = 3.4

OTHER INFORMATION: SWISSPROT HIT: Q98936, EVALUE 1.80e+00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GVSESDGDEYAMASSAESSPGEYEWEYDEEEEKNQLEIERLEEQ 104
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                                                                                                                APPLICATION NUMBER: 2001-01-30
FILING DATE: 2001-01-30
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
TITING DATE: 2001-01-30
TITING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
                                                       PPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/USO1/00663
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00661
                                                                                                           APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21 PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30
     APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2001-01-30
                                                                             ILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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474 IMQNWARIEARLCNNMQKARELWDSIMTRGNAKYAN-MWLEYYNLERAHGDTQHCRKALH 532
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09978242
Patent No. US200200098566A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 714 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                   634 -----GDDEEEQPS 642
                                                                                                                                                                                                                                                                                                            659 EEYFDYIFPEDAANOPN 675
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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US-09-978-242-3
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LOCATION: (153)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (229)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-301-1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 ESDGDEYAMASSAESSPGEYEWEYDEEEEKNQLEI------ERLEE-QLSINVYDY 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 NCHVDL-----IRLLRLEGELTKVRMAR---QKMSEIFPLTEELWLEWLHDE----IS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 ALDVDYRNITLWLKYAEMEMKNRQVXHARNIWDRAITTLPRVNQFWYKYTYMEEMLGNVA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 MAQDGLDREHVYDLFEKAVKDYICPNIWLEYGQYSVGGIGQKGGLEKVRSVFERALSSVG 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 WSEDPIPESVIQNYNKALQQLEKYKPYEEALLQAEAPRLAEYQAYIDFEMKIGDPARIQL 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 708;
                                                               APPLICANT: Rosen et al. TILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
4.5%; Score 225; DB 10; 3
Best Local Similarity 19.7%; Pred. No. 2.5e-06;
Matches 145; Conservative 125; Mismatches 279;
                                                                                                      FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/USO0/05882
PRIOR PELING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
Sequence 1012, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
                                                                                                                                                                                                                                                                                        SEQ ID NO 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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                                                                                       583 AAEKEAALV-----QQEEEKAEQRKRARAEK---KALKKKKIRGPEKRGADEDDEKEW
                                                      533 RAVQCTSDYPEHVCEVLLTMER-----TEGSLEDWDIAVQKTETRLARVNEQRMK---
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4.5%; Score 224.5; DB 10; Length 714;
Best Local Similarity 23.5%; Pred. No. 2.7e-06;
Matches 94; Conservative 67; Mismatches 134; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coriey, Neil C. Shah, Purvi rITLE OF INVENTION: HUMAN NUCLEOLIN-LIKE PROTEIN NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - ATTORNEY/AGENT INFORMATION:
NAME: B1111ngs, Lucy J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0451 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/978,242
FILING DATE: 15-Oct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/241,333
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: 08/990,114
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APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               HER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
HER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
HER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
HER INFORMATION: EXPRESSED IN HOR MARROW, SIGNAL = 1.2
HER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
HER INFORMATION: EXPRESSED IN HEATA, SIGNAL = 1.5
HER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 1.5
HER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 1.7
HER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
HER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
HER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
HER INFORMATION: EXPRESSED IN HIT: 032866, EVALUE 6.100+00
HER INFORMATION: EXT. HUMAN HIT: AU143744.1, EVALUE 1.00e-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 MEATFAEYEEWSEDPIPESVIQNYNKALQQLEKYKPYEEAL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 34622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 4.2%; Score 208.5; DB 9; Best Local Similarity 19.6%; Pred. No. 0.0001; Matches 213; Conservative 170; Mismatches 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.3%; Score 217; DB 10;
100.0%; Pred. No. 2.2e-07;
tive 0; Mismatches 0;
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CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR PLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 164, Application US/10171311 Publication No. US20030087270A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen, Yan
Zhao, Xumei
Monahan, John
Kamatkar, Shubhangi
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Best Local Similarity 100.0
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: MRI-035
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                       ASEDEDEREDEREREDEREDDEREEDDOSEEERAMEITPAKGKKAPAKVVPVKAKNVAEEDDDDE 246
                                                                                                                                                                                                                                                                             306 TPFNLFIGNLNPNKSVAELKVAISEPFAKNDLAVVDVRTGTNRKFGYVDFESAEDLEKAL 365
                                                                                                                                                                                                                                                                                                                                 SL------KRDMPKVLHDSSK--DSITVFVSNLPYSMQEPDTKLRPLFEACGEVVQ 734
                                                                                                                                                                                                                                                                                                                                                                                                                                            735 IRPIFSNRGDFRGYCYVEFKEEKSALQALEMDR-KSVEGRPMFVSPCVDKSKNPDFKVFR 793
                                                                                                              -----PSKRRR---VENSIPAAGETQNVE----
                                                                                                                                             : | |:||: | 247 EEDEDEBEBEBEBEBEBEBEBEBPVKPAPGKRKKEMTKQKEVPEA-KKQKVEGSEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    794 YSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTNRAGKPKGLAYVEYENESQ
                                                                                                                                                                                                                         --VAAGPAGK--CAAVDVEPPSKQK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     854 ASQAVMKMDGMTIKENIIKVAISNPPQRKVPEKPETRKAP 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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Patent No. US20020048763A1
AAEKEAALVQQEEEKAEQRKRARAE
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QO	ILVMDDQ	Db 1881 QLKRQLE
Qy	59EEGVSESDGDEYAMASSAESSPGEYEWEYDEEEEKNOLE 97	RESULT 9
qq	994 NNKLSKERKLLEERISDLTTNLAEBEEKAKNLTKLKNKHESMISELEVRL-KKEEKSRQE 1052	US-U9-92/-29/-2 ; Sequence 2, Applicat
Οy	98 IERLEEQLSINVYDYNCHVDLIRLEGELTKVRMARQKMSEIFPLTEELWLEWLHDEI 157	; Fublication No. USZU; GENERAL INFORMATION:
QQ	RKLEGDASDFHEQIADLQAQIA	; APPLICANI: MAILK, F ; APPLICANI: Beraud,
Qy	158 SMAQDGLDREHVYDLFEKAVKDYICPNIWLEYGQYSVGGIGQKGGLEKVRSVFER 212	; APPLICANT: Freeuma ; APPLICANT: Craven,
QΩ	1104 AQKNNALKKIRELEGHISDLQEDLDSERAARNKAEKQKRDLGEELEALKTELED 1157	; APPLICANT: SAKOWIC ; APPLICANT: Hartman
0y	213 ALSSVGLHMTKGLALWEAYREFESAIVEAARLEKVHSLFRRQLAIPLYDMEATFAEYEEW 272	; FILE REFERENCE: CYT
qq	1158 TLDSTATQQELRAKREQEVTVLKKALDEFTRSHEAQVQEMRQK 1200	CURRENT FILING DATE
Qy	273 SEDPIPESVIQNYNKALQQLEKYKPYEEALLQAEAPRLAEYQAYIDFEMK- 322	SOFTWARE: FastSEQ f
οg	1201 HAQAVEELTEQLEQFKRAKANLDKNKQTLERENADLAGELRVLGQAKQEVEHKKK 1256	; SEQ ID NO 2 ; LENGTH: 1945 . myde. ppm
Qy	323CLVPDLWIRYSQ 352) TIPE: FRI ; ORGANISM: Human
qq	1257 LEAQVQELQSKCSDGERARAELNDKVHKLQNEVESVTGMLNEAEGKAIKLAKDVASLSSQ 1316	7-160-176-60-60
οy	353 YLDRQLKVKDLVLSVHNRAIRNCPWTVALWSRYLLAMERHGVDHQVISVT 402	arcn Sal Simi
qq	1317 LQDTQELLQEETRQKLNVSTKLRQLEEBRNSLQDQLDEEMEAKQN 1361	Matches 2
ολ	403 FEKALNAGFIQATDYVEIWQAYLDYLRRRVDFKQDSSKELEELRAAF-TRALEYLK-QEV 460	Qy 6 ETSASEPE ::
g		Db 942 EDRGQQLQ
	FERFNESGDDSCVIMONWARIEARLONNMOKARELWDSIMT	Qy 59
	NORTH STATE OF THE	Db 1001 NNKLSKER
3 8	ANNALES ENVAITED BY STOWN TO BY STOWN TO STOWN T	Qy 98 IERLEEQL
5 E	ADEKEPRALGIADA IFPARET PARET FORMER KARMENT VECKNANDET FREEDA	Db 1060 LEKLKRKL
3 8	CIVEN EL LANDES NOTES DIVERSE DE L'ANTIGNE D	Qy 158 SMAQDGLD
s ස	LI-MEKTEGSLEDWILAVQXTETKLAKVREÇKMKAAEKEAALVQQ I II : : III I I I I I I I	: : : Db 1111 AQKNNALK
a :	EIQMEEMATIQLEELEDELELQATEDAARAKUEVAMQALAGQKEKULQAKUEQNEERKKQLQKQ	Qy 213 ALSSVGLH
÷ €		Db 1165 TLDSTATQ
3 3		Qy 273 SEDPIPES
; f	1658 OPETERAGE PROPERTY OF THE STATE OF THE	Db 1208 HAQAVEEL
3 8	VALUEDENTANONDELT OLGANENENANGODENDENYUNE DEARGENANNYA- UERREE VANDENANGOT VERNINDIVIT IIRGGARG TRUTHIGAN DA GAADRAMAT DAT DESAAGAIRIAAT DA	Qy 323
S 2		Db 1264 LEAQVQEL
3 3	DABELBASSUSG - KNALKU - ENKREBERTAQLEEEEEEEEGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Qy 353 YLDRQLKV
r c	SNKGDFKGICIVEFKEEKSALQALEMHKKSVEGRFMFVSPCVDKSRNPDFKVFRYSTSLE	: Db 1324 LQDTQELL
a :	SN	Qy 403 FEKALNAG
S 8	OUG NHRAFISGAFFSCTREELEEELCRAHGIYKDAKLYTNRAGKPKGLAYYEXENEGQA 834	Db 1369 LERHISTL
3 8	ANDERVOLVE STATEMENT TO THE TOTAL TO	Qy 461 EERFNESG
s 음	OJJ SZAVNIKUCHITINGALINYALSNIFUGURVEREETIRAAFGGFMLLFUTTGARGNGKTULLS 9.14 1840 ATKSLKQKDKKLKEILLLQVEDERRMAEQYKEQAEKGNARYK 1880	Db 1429 KNRLQQEL
ł		Qy 507 YANMWLEY

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ty 19.6%; Pred. No. 0.0001;
ervative 170; Mismatches 399; Indels 305;
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ud, Christophe
edman, Richard
wicz, Roman
man, James
CYTOP018
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TE: 2001-08-10
NOS: 17
for Windows Version 4.0
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0030032018A1
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2 921
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6 ETSASEPEAESKAGPKADGEEDEVKAARTRRKULSRAVAAATYKTWGPAWDQQ 58 :	461 EERFNESGDPSCVIMONWARIEARLCNNMQKARELWDSIMT	855 SQAVMKMDGMTIKENIIKVAISNPPORKVPEKPETRKAPGGPMLLPOTYGARGKGRTQLS 914 : : : : : : : : : : : : 1840 ATKSLKQKDKKLKEILLQVEDERKMAEQYKEQAE
	6 6	Qy Dp
1485 AREKETKALSLARALEGALEAKEELERTUKMIKAEMEDLVSSKDDVGKNVHELEKSKRAL 1544 Cy 550 LT-MERTEGSLEDWDIAVQKTETRLARVNEORMKA	RESULT 10 1S-10-171-311-162 1S-20-171-311-162 1S-20-171-311-162 1S-20-171-311-162 1S-20-20-20-20-20-20-20-20-20-20-20-20-20-	Query Match 4.2%; Score 208.5; DB 9; Length 1972; Best Local Similarity 19.6%; Pred. No. 0.0001; Matches 213; Conservative 170; Mismatches 399; Indels 305; Gaps 44;

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1720 LAEELASSLSG--RNALQD-EKRRLEARIAQLEEELEEEQGNMEAMSDRVRKATQQAEQL 1776
  1485 AREKETKALSLARALEEALEAKEELERTNKMLKAEMEDLVSSKDDVGKNVHELEKSKRAL 1544
                                                                                                   1545 ETQMEEMKTQLEELEDELQATEDAKLRLEVNMQALKGQFERDLQARDEQNEEKRRQLQRQ 1604
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1605 LHEYETELEDERKQRALAAAAKKKLEGDLKDLELQADSAIKGREEAIKQLRKLQAQMKDF 1664
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                                                                                                                                                       -----EEEKAEQRKRARAEKK-------ALKKKKKIRGPEKRG
                                                                                                                                                                                                                                                       ADEDDEKEWGDDE-----EEQPSKRRRVENSIPAAGETQNVEVAAGPAGKCAAVDVEPPS
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
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4.1%; Score 206.5; DB 10;
Best Local Similarity 22.6%; Pred. No. 2.4e-05;
Matches 76; Conservative 65; Mismatches 134;
                                                    550 LT-MERTEGSLEDWDIAVQKTETRLAR--VNEQRMKA-
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NUMBER OF SEQ ID NOS: 440
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 234
LENGTH: 494
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APPLICANT: Wang, Tongtong
APPLICANT: Secrist, Heather
APPLICANT: Mohamath, Raodoh
APPLICANT: Indirias, Carol Y.
APPLICANT: Fan, Liqun
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US-09-833-790-234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 LQDTQELLQEETRQKLNVSTKLRQLEE------ERNSLQDQLDEEMEAKQN 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IERLEEQLSINVYDYNCHVDLIRLLRLEGELTKVRMARQKMSEIFPLTEELWLEWLHDEI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 SEDPIPESVIQ-----NYNKALQQLEKYKPYEEALLQAEAPRLAEYQAYIDFEMK- 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1979;
                                                                                                                                                                                                                APPLICANT: Malik, Fady
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
APPLICANT: Treedman, Richard
APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Hartman, James
TITLE OF INVENTION: Human smooth muscle myosin heavy chain
FILE REFERENCE: CYTOPO18
CURRENT APPLICATION NUMBER: US/09/927,597
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.2%; Score 208.5; DE Best Local Similarity 19.6%; Pred. No. 0.0001
                                                                                                                                          Sequence 4, Application US/09927597 Publication No. US20030032018A1 GENERAL INFORMATION:
| | |:
1881 QLKRQLE 1887
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ORGANISM: Human
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APPLICANT: Gatanaga, T.
APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
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566 GGRKLERARDLFEQALDGCPPKYAKTLYLLYAQLEEEWGLARHAMAVYERATRAVEPAQQ 625
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                                                                                                                                                                                                                                                                                                                                                                                                        387 ATGKPHTLWVAFAKFYEDNGQLDDARVILEKATKVNFKQVDDLASVWCQCGELELRHENY 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :: | | |::|:|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |:|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |:|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |:|| |::|| |::|| |::|| |::|| |:|| |::|| |:|| |:|| |:|| |:|| |::|| |:|| |:|| |:|| |:|| |:|| |:||
   216 QLWHE-LCDLISQNPDKVQSLNVDAIIRGGLTRFTDQLGKLWCSLADYYI----RSGHFE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          594 EEEKAEQRK----RARAEKKALKKKKKIRGPE--KRGADEDDEKEWGDDEEEQPSKRRRV 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447 DEALRLIRKATALPARRAEYFDGSEPVQNRVYKSLKVWSMLADLEESLGTFQSTKAVYDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      680 RARAIYSFCSQICDPR-----TTG----AFWQTWKDFEVRHGNEDTIKEMLRIRRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         536 QCTSDYPEHVCEVLLIMERTEGSLEDW--DIAVQKTETRLARVNEQRMKAAEKEAALVQQ
                                                                  205 KVRSVFERALSSVGLHMTKGLALWEAYREFESAIVEAARLEKVHSLFRRQLAIPLYDMEA
                                                                                                                                                                                                    -----EWSE----DPIPESVIQNYNKALQQLEKYK
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APPLICATION NUMBER: US/09/984,198
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 EEAL----LOAEAPRLAEY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 153, Application US/09984198
Patent No. US20020106679A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 GVDH-QVISVTFEKALN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
                                                                                                                                                                                                    265 TFAEYE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  838 QOSVPAA 844
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                                                                                                                                                                                                                                                                                                                                     297 P----
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Patent No. US20020091243A1
GENERAL INFORMATION:
APPLICANT: Grange, T.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
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   -- DRKLFVGMLNKQQSEDDVRRLFEAFGN 166
                                                               827 VKDLRLVTNRAGKPKGLAYVEYENESQASQAVMKMDG---MTIKENIIKVAISNPPQRKV 883
                                                                                                     227 MRRMQQMAGQMGMFNPMAIPFGAYGAYAQALMQQQAALMASVAQGGYLNPMAAFAAAQMQ 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 ELWLEWLHDEISMAQDGLDREHVYDLFEKAVKDYI--CPNIWLEYGQYSVGGIGQKGGLE
                                                                                                                                                                                                884 PEKPETRKAPGG---PMLLP-QTYGARGKG--RTQLSLLPRALQ----RPSAAAPQAE--
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                                                                                                                                                                                                                                                                                                                                     932 -----NGPAAA------949
                                                                                                                                                                                                                                                                                                                                                                                                    287 OMAALNMNGLAAAPMTPTSGGSTPPGITAPAVPSIP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
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APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
120 TLPGMNRPIQVKPADSESRG----
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REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22(
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154
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Matches 136; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS: sir
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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US-09-752-639-153
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Sequence 16, Application US/09969384
Publication No. US20020192749A1
GENERAL INFORMATION:
APPLICANT: MOORE, et al.
TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 LLPPPPQQKITDEEELNDYKLRKRTFEDNIRKN---RTVISNWIKYAQWEESLKEIQRA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 R---QKMSEIFPLTEELWLEWLHDEISMAQDGLDREHVYDLFEKAVKDYICPN-IWLEYG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIPESVIQNYNKALQQLEKYKPYEEALLQAEAPRLAEYQAYIDFEMKIGDPARIQLI--- 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 FVRVRVIYKY--ALDRISNKMPKNSLKI---IPSLRR-----SLVIGGVLKISIVSKR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     435 LGTSIGKCPKNKLFKVYIELELQLREFDRC----RKLYEKFLEFGPENCTSWIKFAELE 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---FERALVENCLVPDLWIRYSQYLDRQLKVKDLVLSVHNRAIRNCP------WT--VA 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AASTAAGKQRIPKVAKVKNKAPAEVQITA------EQLLRE-----AKERELE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 AGPKADGEEDEVKAARTRRKVLSRAVAAATYKTMGPAWDQQEEGVSESDGDEYAMASSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 SSPGEYEWEYDEEEEKNQLEIER---LEEQLSINVYDYNCHVDLIRLLRLEGELTKVRMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSIYERALDVDYRNITLWLKYAEMEMKNRQ - - - - VTHARNIWDRAITTLPRVNQFWYKY -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 VVLVHPDVKNWIKYARFEEKHAYFAHARKVYERAVEFFGDEHMDEHLYVAFAKFEENQKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381 LWSRYLLAMERHGVD----HQVISVTFEKALNAGFIQATDYV----EIWQAYLDYLRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               432 VDF---KQDSSK-----ELEELRAAFTRALEYLKQEVEERFNESGDPSCVIMQNWARIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 ARLCNNMOKARELWDSIMTRGNAKYAN-MWLEYYNLERAHGDTQHCRKALHRAVQCTSDY
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                                                                                                                                                                                                                                                               FILE REFERENCE: PT055P1
CURRENT APPLICATION NUMBER: US/09/969,384
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10542
PRIOR FILING DATE: 2001-04-02
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
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PRIOR FILING DATE: 2000-04-03
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US-09-969-384-16
                         648 ENSIPAA 654
                                                                838 QOSVPAA 844
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LENGTH: 687
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                                                                                                                                                                                                                                      REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFRAX: 650-494-0792
                                         PCT/US99/10793
                                                                                                                                          FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                 09/081,385
                                                                                                                         08/964,747
                                                                                                                                                                                                                                                                                                                                                                      153:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 852 amino acids
TYPE: amino acid
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Best Local Similarity 20.48
Matches 136; Conservative
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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Qy	542	542 PEHVCEVLLTMERTEGSLEDWDIAVQKT 569	569
qa	546	11 1::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	595
Qy	570	570 ETRLARVNEQRWKAAEKEAALVQQEEEKAEQRKRAR	. 509
qa	296	596LGEVLEBERGTASDKERVDKLMPEKVKKRRKVQTDDGSDAGWEEYFDXIFPEDAANQ 652	652
Qy	909	1	
QQ	653	653 PNLKLLAMAKLWKKQQQEKGDAEHHPDEDVDESE 686	
Search completed: Job time : 60 secs	complet e:60	Search completed: June 18, 2003, 14:01:09 Job time : 60 secs	

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 18, 2003, 13:48:53; Search time 26 Seconds (Without alignments) 3560.671 Million cell updates/sec Run on:

US-09-763-985A-2 4994 1 MATAAETSASEPEAESKAGP......AATEAPKMSNADFAKLFLRK 963 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues

283224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote		⊆	nucleolin - Africa	1	ca]	nuclear localizati	probable cell cycl	nucleolin - chicke	nucleolin - human	nucleolin - mouse	probable nuMl prot	hypothetical prote		. nucleolin - Chines	nucleolin - rat	crooked neck-like	smooth muscle myos	smooth muscle myos	cleavage stimulati	splicing factor U2	hypothetical prote	rnal4 protein - fi	nucleolin homolog	splicing factor -	nucleolin homolog	elav protein - fru	nucleolar protein	conserved hypothet
SUMMARIES	ΙD	T18650	T09890	T39743	S18874	S32644	T31808	A39205	T13427	DNCHNL	A35804	DNMS	A96527	T17297	A40252	A27441	JH0148	T45742	JC5421 .	JC5420	S50852	S22646	T34081	T11668	T06458	I55595	T09648	A33130	S55785	038
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de	Query	17.3	16.5	10.1	6.1	5.9	5.5	5.4	5.4	5.2	4.9	4.9	4.9	4.8	4.5	4.5	4.5	4.5	4.4	4.4	4.3	4.3	4.3	4.3	4.3	4.3	4.2	4.2	4.2	4.2
	Score	864	823	506.5	305	293.5	276.5	272	268.5	S	245.5	244.5	243	239.5	226.5	224.5	224	222.5	217.5	217.5	216.5	216	216	215	214.5	212.5	211	210	209.5	209
	Result No.	1	7	e	4	2	φ	7	œ	6	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	53

hypothetical prote myosin heavy chain	ribonucleoprotein, hypothetical prote	"Myost" meavy charm RNA-binding protei probable splicing	myosin alpha beavy	gene $su(f)$ protein NF-180 - sea lampr	splicing factor U2 hypothetical prote	myosin heavy chain slow myosin heavy	nucleic acid-bindi
T01563 A33977	S22548 T47673	S50765	138055	A46389 I51116	S20250 T33022	I48175 A59234	S23780
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ALIGNMENTS

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Amalric,

number: S30250; MUID:93181171; PMID:8441611

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-651 <RAN>
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                                                               72
                                                                                       142 FPLTEELWLEWLHDEISMAQDGLDREHVYDLFEKAVKDYICPNIWLEYGQYSVGGIGQKG
                                                                                                      -----GLEKVRSVFERALSSVGLHMTKGLALWEAYRE----FESAIVEAARLE
                                                                                                                                                                                            -----KVHSLFRRQLAIPLYDMEATFAEY----EEWSEDPIPESVIQNYNKALQQLEK
                                                                                                                                                                                                                                               --YKPYEEALLQAEAPRLAEYQAYIDFEMKIGDPAR-----IQLIFERALVENCLVP
                                                                                                                                                                                                                                                                       252 RNAKIFNKELLLNSANHSLE--AYMDL---INDESRRSTAELQYITTLYERAIVLYPLIP
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ilarity 22.2%; Pre
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nucleolin - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Nenopus laevis (African clawed frog)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S30250; A30166; S18874
R;Rankin, M.L.; Heine, M.A.; Xiao, S.; LeBlanc, M.D.; Nelson, J.W.; DiMario, Nucleic Acids Res. 21, 169, 1993
A;Title: A complete nucleolin cDNA sequence from Xenopus laevis.
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A;Title: Nucleolin from Xenopus laevis: cDNA cloning and expression during developmen A;Reference number: A30166; MUID:89252811; PMID:2656405
A;Accession: A30166
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 126-214, 0, 216-218, LR., 221-410, 0, 412-580, E, 582-651 <CAI>
C;Superfamily: nucleolin; ribonucleoprotein repeat homology
C;Superfamily: nucleolin; ribonucleoprotein repeat homology KRMAI>
F;326-389/Domain: ribonucleoprotein repeat homology KRMAI>
F;36-389/Domain: ribonucleoprotein repeat homology KRMA>
F;504-568/Domain: ribonucleoprotein repeat homology KRMA>
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: I51619; S32644
R;Messmer, B.; Dreyer, C.
Bur. J. Cell Biol. 61, 369-382, 1993
A;Title: Requirements for nuclear translocation and nucleolar accumulation of nucleol A;Reference number: I51619; MUID:94039235; PMID:8223724
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A;Cross-references: EMBL:X63091; NID:964936; PIDN:CAA44805.1; PID:964937
R;Caizergues-Ferrer, M.; Mariottini, P.; Curie, C.; Lapeyre, B.; Gas, N.;
Genes Dev. 3, 324-333, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.1%; Score 305; DB 2; 26.5%; Pred. No. 7.7e-09;
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0y 631	EEEEDDSDEEDQKPIKKPIAKKAVAKKEESEEDDEDEDESEEKPVAKRPLAKNPPVK 156	Qy
Oy 665 GPAGKCAAV	-KEWGDDEEEQPSKRRRVENSIPAAGETQNVEVAA 664	qa
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Oy 697 HDSSKDSITVFYSNLPYSMQEPDTK Db 277 TDTASEGFSIFIGNLNSTLDFDELK Oy 755 EEKSALGALEMDRKSVEGRPWFVSPR Db 333 SEBEVEKLLSGKKILGLEVTNRE OY 813 TKEELEEICKAHGTVKDLRLYTNRE OY 873 VAISNPPORKVPEKPETRKAPG Db 388 SAEELGEIFENAKDIRIPTGND OY 873 VAISNPPORKVPEKPETFKAPG T31808 Hypothetical protein M03F8.3 - Caenorhal C; Specias: Caenorhabditis elegans C; Date: 29-Oct-1999 #sequence_revision C; Accession: T31808 RDA445050, S.; Wohldmann, P. RDA46505. S.; Wohldmann, P. RDA46505. S.; Wohldmann, P. RDA46505. S.; Wohldmann, P. RDA46505. T31808 RSDA46505. S.; Wohldmann, P. RSDA4COSSION: T31808 RSDA46505. S.; Wohldmann, P. RSDA4COSSION: T31808 RS	AQKGKKTAPAKAEDBDDDDDDDDDDDDDDEDDEEDDDDEQQGPAKRKKEMPKNNVPEAKKTK 276	Qy
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OY 755 EEKSALQALEMDRKSVEGRPMFVSP 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TOTASEGFSIFIGNINSTLDFDELKDALREFFSKKNLTIQDVRIGGSKKFGYVDFS 332	Qy
Db 333 SEEVEKALKLSCKKIIGLEVITER OY 813 TREELERICKAHGTVKDLRLYTURBA :	IDRKSVEGRPMFVSPCVDKSKNPDFKVFRYSTSLEKHKLFISGLP	qa
QY 813 TREELEBICKAHGTVKDLRLVTNRAA	SEEEVEKALKLSGKKILGLEVKIEKAVAFDKNKNAENKKERDSRTLFVKNIPYST 387	δλ
Db 388 SABELGETH:	TKEELEEICKAHGTVKDLRLVTNRAGKPKGLAYVEYENESQASQAVMKMDGMTIKENIIK 872	QQ
Qy 873 VAISNPPORKVPEKPETRKAPG By 445 VDFTGEKSQNSGGRRGPAN RESULT 6 T31808 hypothetical protein M03F8.3 - Caenorhai C: Species: Caenorhabditis elegans C: Date: 29-Oct-1999 #sequence_revision C: Accession: T31808 R: Davidson, S: Wohldmann, P. R: Status: prelliminary: translated from (A: Molecule type: DNA R: Steenere undner: 221089 A: Status: prelliminary: translated from (A: Molecule type: DNA R: Steenere number: 271089 A: Status: prelliminary: translated from (A: Molecule type: DNA R: Coos-references: EMBL: AF016441; PIDN A: Experimental source: strain Bristol N: A: Gene: CESP: M03F8.3 A: Map position: 5 A: Mintons: 43/3; 388/3; 459/3; 632/2 C: Superfamily: Schizosaccharomyces pomb Query Match Best Local Similarity 19:3%; Pred. Matches 152; Conservative 132; Mil Db 19 RAAKVRNKSFADFINSKVNITY-F: Oy REWENDEEEERNQLEIERLEEQLSIN Db 78 PDELKEYQRKRKEEE		ζŎ
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RESULT 6 T31808 hypothetical protein M03F8.3 - Caenorhal C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T31808 R;Davidson, S.; Wohldmann, P. R;Reference number: 221089 A;Reference number: 221089 A;Reference number: 221089 A;Redence preliminary; translated from A;Rolecule type: DNA A;Redence type: DNA A;Reperimental source: strain Bristol N; C;Genetics: A;Map position: 5 A;Map position: 5 A;Map position: 5 A;Introns: 43/3; 388/3; 459/3; 632/2 C;Superfamily: Schizosaccharomyces pombourp Match Best Local Similarity 19.9%; Pred. Matches 152; Conservative 132; Mil Db 19 RAAKVENEVELEBRIEBEQLSIN ON 84 EWEVDEBEERNQLEIBRIEBEQLSIN Db 78 PDELKEYQRKRKEREF	EKSQNSGGRRGPAG 463	Qy
hypothetical protein M03F8.3 - Caenorhal hypothetical caenorhabditis elegans C: Species: Caenorhabditis elegans C: Species: Caenorhabditis elegans C: Species: Caenorhabditis elegans C: Species: T31808 R: Davidson, S: Wohldmann, P. Submitted to the EMBL Data Library, Jul. A: Description: The sequence of C. elegans, Received communer: 221089 A: Received communer: 221089 A: Status: preliminary: translated from A: Status: preliminary: T61 CDAV> A: Cross-references: EMBL:AF016441; PIDN A: Experimental source: strain Bristol N: A: Gene: CESP: M03F8.3 A: Matches: 152: Conservative 132; Millarity: Millarity: 19.3%; Pred. Matches: 152; Conservative 132; Milli:: 1 Db 19 KAAKVENKVSFADFINSKVNITY-F: Oy 84 EWEVDEEEEKNQLEIERLEEQLSIN Db 78 PDELKEYQREKEEE		qa
C. Species: Caenorhabditis elegans C. Date: 29-Oct.1999 #sequence_revision C. Accession: Tay1808 R. Bavidson, S.; Wohldmann, P. Submitted to the EMBL Data Library, Jul. A. Description: The sequence of C. elegan A. Reference number: 221089 A. Accession: T31808 A. Molecule type: DNA A. Residues: 1-761 ADAV A. Cross-references: EMBL.AF016441; PIDN A. Cross-references: EMBL.AF016441; PIDN A. Cross-references: EMBL.AF016441; PIDN A. Genetics: A. Genetics: A. Genetics: A. Genetics: A. Genetics: C. Superimental source: strain Bristol N C. Genetics: A.		δδ
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A Description: The sequence of C. elegan A, Reference number: 221089 A; Status: preliminary: translated from A; Molecule type: DNA A; Residuale to Surce: strain Bristol N; Experimental source: strain Bristol N; A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: Survivality: Solizosacharomyces pomboup the constraint of Sisterial N; Schizosacharomyces pomboup the constraint of Sisterial N; Schizosacharomyce special Similarity 19:3%; Pred. Matches 152; Conservative 132; Miscophilia Sisterial N; Schizosacharomyces Sisterial N; Schizosacharomyces Sisterial N; Schizosacharomyces Sisterial N; Schizosacharomyces Sisterial S	n, P. ta Library, July 1997	RESUL
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A; Molecule type: DNA A; Residues: 1.761 CDAV> A; Cross-references: EMBL; AF016441; PIDN A; Cross-references: EMBL; AF016441; PIDN A; Genetics: C; Genetics: A; Gene: CESP: M03F8.3 A; Map position: 5 A; Introns: 43/3; 388/3; 459/3; 632/2 C; Superfamily: Schizosaccharomyces pomb Query Match Best Local Similarity 19.9%; Pred Matches 152; Conservative 132; Mil Db 19 KAAKVKNKVSPADFINSKVNITY-F; Oy 84 EWEYDEEEEKNQLEIERLEEQLSIN Db 78 PDELKEYQRKKREFE	ranelated from CD/DNDI/DDDI	8,0
A. Cross-references: EMBL.AF016441, PIDN A. Experimental source: strain Bristol N. C. Genetics: A. Genetics:		C; Acc
Genetics: A;Gene: CESP: M03F8.3 A;Gene: CESP: M03F8.3 A;Introns: 43/3; 388/3; 459/3; 632/2 A;Introns: 43/3; 388/3; 459/3; 632/2 C;Superfamily: Schizosaccharomyces pombo Ouery Match Best Local Similarity 19.9%; Pred. Matches 152; Conservative 132; Min Oy 30 KAARTRRKVLSRAVAAATYKTJ Db 19 KAAKVKNKVSFADFINSKVNITY-F. Oy 84 EWEYDEEEEKNQLEIERLEEQLSIN Db 78 PDELKEYQRKKREFE	:AF016441; PIDN:AAB65909.1; GSPDB:GN00023; CESP:M03F8.3	, , , ,
A, Map position: 3 A, Introns: 43/3; 388/3; 459/3; 632/2 A, Introns: 43/3; 388/3; 459/3; 632/2 C, Superfamily: Schizosaccharomyces pombo Query Match Best Local Similarity 19.9%; Pred. Matches 152; Conservative 132; Mis Qy 30 KAARTRRKVLSRAVAAATYKTI Db 19 KAAKVKNKVSFADFINSKVNITY-F; Qy 84 EWEYDEEEEKNOLEIERLEEQLSIN Db 78 PDELKEYQRKKREFE		A; R
C; Superfamily: Schizosaccharomyces pombo C; Superfamily: Schizosaccharomyces pombo C Superfamily: Schizosaccharomyces pombo Schizosaccharomyces pombo Schizosaccharomyces pombo Schizosaccharomyces Score Best Local Similarity 19:4%; Pred. Matches 152; Conservative 132; Mis Mischell Schizosaccharomyces Schi	450/3. 632/3	A; Acc
Ouery Match Best Local S Matches 152 30 19 84 78	charomyces pombe hypothetical protein SPBC31F10.11c	A; Kes
30 19 84 78	5.5%; Score 276.5; DB 2; Length 761; 19.9%; Pred. No. 3.1e-07; ative 132; Mismatches 268; Indels 211; Gaps 31;	Gene A;Tit A;Ref
19 84 78	LSRAVAAATYKTMGPAWDQQE	A; Ac
84		A; Kes A; Cro
78	EWEYDEBEBENQLEIBRLEBQLSINVYDYNCHVDLIRLRLEGELT 129	R;Ska Yeast
	DGIRKNRMQLANWIKYGKWEESI	A;Tit

Terrate names: nucleolar protein NSR1: yeast (Saccharomyces cerevisiae) lternate names: nucleolar protein NSR1; p67 protein; protein G7001; protein YGR159 pecies: Saccharomyces cerevisiae
http://doi.org/10.1001/10.

sidues: 1-414 <LEE>

ross-references: GB:X57185; NID:g4057; PIDN:CAA40472.1; PID:g4058
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blecule type: mRNA studes: 155-414 GAM-coss-references: EMBL:X57185 bte: The authors translated the codon TTC for residue 188 as Arg, GGT for residue atal, J: Nawrock!, A.; Goffeau, A. st 11, 1421-1427, 1995 ttle: The sequence of a 27 kb segment on the right arm of chromosome VII from Sacc

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A; Cross-references: SMBL:AL009195; NID:e1355203; PID:e1248582; PIDN:CAA15705.1
R; Zhang, K.; Smouse, D.; Perrimon, N.
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A; Title: The crooked neck gene of Drosophila contains a motif found in a family of ye A; Reference number: A39634; MUID:91257574; PMID:2044955
A; Accession: A39634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 KDRTQE-------LFKAYTKHEKKYGDRAGIEDVIVSKRKYQYEQEVAANPTNYD 326
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A; Description: Sequencing the distal X chromosome of Drosophila melanogaster. A; Reference number: 217668 A; Accession: T13427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: EG:30B8.1
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC31F10.11c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 FV--YVHDDVKNMIKFARFE----ESHGFIHGSRRVFERAVEFFG------DDYIE
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                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-702 <MUR>
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A;Cross-references: FlyBase:FBgn0000377
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A;Molecule type: mRNA
A;Residues: 1-702 <ZHA>
A;Cross-references: GB:X58374
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A. Residues: 1-414 < VAN>
A. Residues: 1-414 < VAN>
A. Residues: 1-414 < VAN>
A. Coss. references: RBHI: 272944; NID: 91323270; PIDN: CAA97173.1; PID: e243542; PID: 9132327
A. Cross references: BHI: 222944; NID: 91323270; PIDN: CAA97173.1; PID: e243542; PID: 9132327
A. Cross references: Stain S288C
R; Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
A. Reference number: S64071
A. Accession: S64470
A. Molecule type: DNA
A. Reference number: S64071
A. Molecule type: DNA
A. Residues: 1-188 < RIE>
A. Cross-references: EMBL: 272944; MIPS: YGR159C
A. Cross-references: EMBL: 272944; MIPS: YGR159C
C. Senerimental source: strain S288C
C. Senerimental s
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                                                                                                                                                                       A)Crossreferences: EMBL:X85807; NID:g1045249; PIDN:CAA59817.1; PID:g1045265
A)Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995
R;Van Dyck, L.; Skala, J.; de Wergifosse, P.; Purnelle, B.; Talla, E.; Nawrocki, A.; submitted to the Protein Sequence Database, May 1996
A;Reference number: S64428
A;Accession: S64468
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113427
probable cell cycle control protein crn - fruit fly (Drosophila melanogaster)
C; Species: Drosophila melanogaster
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 06-Oct-2000
C; Accession: T13427; A39634
R; Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   606 -----AEKKALKKKKIRGPEKRGADEDDEKEWGDDEEEQPSKRRVENSIPAAGET
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                                                                                 Status: nucleic acid sequence not shown; translation not shown; Molecule type: DNA; Residues: 1-414 <SKA>
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    Reference number: S60435; MUID:96158062; PMID:8585325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || : :| || || RGG----SRGFGGRGGGR 366
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Db 612 MQKVMDKMPRRIKKRQKIVSDNGVEE-GWEEVFDYIFPEDEMARPNLKLLAAAK 664	KEWGDDEEEQPSKRRRVENSIPAAGETQNVE
Qy 656 ETQNVEVAAGPAGKCAAVDVEP 677	Db 209 ATPAKAKAESEDEEDEEDEDEEDEEDEEDEESEDEEKPVKEAPGKRKKEMANKSAPE 268
Db 665 MWKTQKDNTVDDPPATAIASEPEP 688	Qy 670 CAAVDVEPPSK 690
	- Db, 269 AKKKKTETPASAFSLFVKNLTPTKDYEELRTAIKEFFGKKNLQVSEVRIGSSKRFGYUDF 328
	Qy 691DMPKVL
NyAlternate names: nucleolar protein C23	Db 329 LSAEDMDKALQLNGKKIMGLEIKLEKAKSKESLKENKKERDARTLFVKNLPYRVTEDE 386
C;Species: Galius gailus (chicken) C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999	Oy 722 LRPLFEACGEVVQIRPIFSNRGDFRGYCYVEFKEEKSALQALEMDR-KSVEGRPMFVSPC 780
C:Accession: S08414; S10766; A32725; I50397; B30099 R;Maridor, G.; Nigg, E.A.	387
Nucleic Acids Res. 18, 1286, 1990 . A:Title: cDNA sequences of chicken nucleolin/C23 and NO38/R23. two major nucleolar prote	VINCENDIDEVUDDVENCT FRUIT DIECT DECCHARDI PETCKALICHUNDT DI VANDACKD
A:Reference number: S08414; WUID:90206792; PMID:2320420 A:Accession: S08414	
A, Status: translation not shown	*** GENOUVESUN GGGENESNILLIVNNESIAASEEILVELKINNISIN FFUNNGGNE
A; Molecule Lype: mkNA A; Residues: 1-694 <mar></mar>	Qy 841 KGLAYVEYENESQASQAVWKMDGMTIKENIIKVAISNPPQRKVPEKPETRKAPGGPMLLP 900
A:Cross-references: EMBL:X17199; NID:g63710; PIDN:CAA35060.1; PID:g63711 R:Maridor, G : Krek, W : Nice R a	FPTAEDAKEALNSCNNTEIEGRAIRLEF
	Qy 901 QTYGARG 907
A; Ille: Structure and developmental expression of chicken nucleolin and NO38: coordinat A; Reference number: S10766; MUID:90304215; PMID:2114180	.
A;Accession: S10766 A;Status: nucleic acid sequence not shown	
A Molecule type: MRNA A Manager 1260. AMPA	RESULT 10
R. Peter, M.; Nakagawa, J.; Doree, M.; Labbe, J.C.; Nigg, E.A.	A35804 nucleolin - human
4	N'Alternate names: phosphoprotein pp100; protein B50; protein C23
A) Reference number: A32725; MUID:90182668; PMID:2178776	C;Species: Homo sapiens (man) C;Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 23-Jul-1999
A;Accession: A32725 A;Molecule type: protein	C;Accession: A35804; S04631; A48138; A55996 R:Grivactava M : McBride O W : Rleming D I : Dollard H B : Burns A I
A; Residues: 56-62;63-109;197-214 <pet></pet>	
K; Borer, R.A.; Lehner, C.F.; Eppenberger, H.M.; Nigg, E.A. Cell 56, 379-390, 1989	A; Title: Genomic organization and chromosomal localization of the human nucleolin gen A; Reference number: A35804: MITD: 90368666: PMTD: 2394707
A; Title: Major Nucleolar Proteins Shuttle between Nucleus and Cytoplasm. A: Reference number: 150397: MITD: 89119560: PMTD: 2914125	A; Accession: A33804
A Accession: 150397	A; Residues: 1-707 <sri></sri>
A;Status: translated from GB/EMBL/DDBJ . A;Molecule type: mRNA	A;Cross-references: GB:M60858; GB:J05584; NID:g189305; PIDN:AAA59954.1; PID:g189306 R:Srivastava: M.: Fleming: P.J.: Pollard: H.: Burns: A.L.
A; Residues: 407-418, 'R', 420-519, 'T', 521-694 <bor></bor>	250, 99-105, 1989
C.Comment: Phosphorylation of this protein by cdc2 kinase may contribute to the reorgani	A;Title: Cloning and sequencing of the human nucleolin cDNA. A;Reference number: S04631; MUID:89290043; PMID:2737305
C;Supertamily: nucleolin; ribonucleoprotein repeat homology C;Keywords: DNA binding: duplication; nucleolus: nucleus: phosphoprotein: RNA binding: t	A;Accession: S04631 A:Status: not compared with conceptual translation
1-247/Domain: acidic <aci> 54-91/Region: 7-residue remeats (M-D-A-K-K-A-IA/XI)</aci>	A; Molecule type: mrnA
254 - 262/Region:	A; Residues: 1-70/ SEKZ> R; Ishikawa, F.; Matunis, M.J.; Dreyfuss, G.; Cech, T.R.
267-275/Region: 282-347/Domain:	Mol. Cell. Biol. 13, 4301-4310, 1993
283-361/Domain: RNA binding #status predicted <rna< td=""><td>(n (n)n) + .</td></rna<>	(n (n)n) + .
372-455/Domain: ilDonucleOpioCein repeat momology 373-448/Domain: RNA binding #status predicted <rnr< td=""><td>A;Accession: A48138 A;Molecule type: protein</td></rnr<>	A;Accession: A48138 A;Molecule type: protein
F;462-525/Domain: ribonucleoprotein repeat homology <rrm3> F;463-538/Domain: RNA binding #status predicted <rna3></rna3></rrm3>	. A;Residues: 458-474 <ish> A:Experimental source: HeLa cell nuclei</ish>
554-618/Domain:	A; Note: sequence extracted from NCBI backbone (NCBIP:134645)
533-634/Domain: kNA binding #Status predicted <kna4> 632-694/Domain: glycine/arginine-rich <grr></grr></kna4>	R;Jordan, P.; Heid, H.; Kinzel, V.; Kuebler, D. Biochemistry 33, 14696-14706, 1994
56,63,70,77,85/Binding site: ph	A; Title: Major cell surface-located protein substrates of an ecto-protein kinase are A; Reference number: A55996; MUID:95086063; PMID:7993898
at(A;Accession: A55996 A:Molecule type: protein
4, Conservative 6	A; Residues: 21-236; 349-362; 399-403; 458-461; 655-656, 'X', 658-660 <jor> A: Experimental source: surface-labelled Refa cells</jor>
OY 583 AAEKEAALV	C; Generican content and the content of the content
Db 149 AAKKSAAAVPAKKPAVVPAKQESEEEEEDDEEDDESEDEEDDESEDEAMDTTPAPVKKPTPAK 208	Cross.
	A) Map postuton: Aque Aquei

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A;Cross-references: GB:M22089; NID:g200111; PIDN:AAA39841.1; PID:g554246 C;Comment: This housekeeping protein is involved in the synthesis, packaging, and mat
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H., Shins, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Mille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A96527
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24.7%; Pred. No. 1.4e-05;
ive 65; Mismatches 138;
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                 preliminary; translated from GB/EMBL/DDBJ
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F;489-494/Region: RNA-binding RNP2 motif
F;524-531/Region: RNA-binding RNP1 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;570-634/Domain: ribonucleoprotein repeat
F;571-576/Region: RNA-binding RNP2 motif
F;607-614/Region: RNA-binding RNP1 motif
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Matches 99; Conservative
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A; Residues: 2-20, 'x', 22-24 < PAS>
R; Yang, T.H.; Tsai, W.H.; Lee, Y.W.; Lei, H.Y.; Lai, M.Y.; Chen, D.S.; Yeh, N.H.; Lee, S
MOI. Cell. Biol. 14, 6068-6074, 1994
A; Title: Purification and characterization of nucleolin and its identification as a tran
A; Reference number: A56240; MUID:94344117; PMID:8065340
A; Accession: A56240
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A;Title: Sequence and structure of the nucleolin promoter in rodents: Characterization A;Reference number: I48118; MUID:89121496; PMID:2906027
A;Accession: 184688
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A.Residues: 1-707 <BOX
A.Residues: 1-707 <BOX
A.COSS.references: GB:X07699; NID:g53453; PIDN:CAA30538.1; PID:g53454
A.COSS.references: GB:X07699; NID:g53453; PIDN:CAA30538.1; PID:g53454
B.Pasternack, M.S.; Bleier, K.J.; McInerney, T.N.
J. Biol. Chem. 266, 14703-14708, 1991
A.Feference number: A40769; MUID:91317840; PMID:1860869
A.Reference number: A40769; MUID:91317840; PMID:1860869
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Afrittle: Structure of the mouse nucleolin gene. The complete sequence reveals
A; Reference number: A29958; MUID:88316930; PMID:3137346
A; Accession: A29958
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267 EEEEEPVKEAPGKRKKEMAKQKAAPEAKKQKVEGTEPTTAFNLFVGNLNFNKSAPELKTG
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                                                        RNA binding
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                                                   nucleolus; nucleus; phosphoprotein;
C; Superfamily: nucleolin; ribonucleoprotein repeat homology C; Keywords: DNA binding; nucleolus; nucleus; phosphoprotein
                                                                             F;308-373/Domain: ribonucleoprotein repeat homology <RRM1>F;394-456/Domain: ribonucleoprotein repeat homology <RRM2>F;487-550/Domain: ribonucleoprotein repeat homology <RRM3>F;573-634/Domain: ribonucleoprotein repeat homology <RRM4>
                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                 4.9%; Score 245.5; DB 2;
llarity 24.2%; Pred. No. 1.3e-05;
Conservative 64; Mismatches 127;
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A; Residues: 2-19;558-567 <YAN>
R; Bourbon, H.
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les 92; Conserv
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A;Status: preliminary A;Molecule type: DNA A:Molecule type: DNA	: : :
A:Gross references: GB:AE005173; NID:g11094815; PIDN:AAG29744.1; GSPDB:GN00141 C:Genetics: A:Genetics: A:Map position: 1	QY 568 KTETRLARVNEQRMKAABKEAALVQOEEERAEQRKRARAEKKALKKKIRGPEKRGADE 627
Query Match 4.9%; Score 243; DB 2; Length 557; Best Local Similarity 24.1%; Pred. No. 1.38-05; Matches 88; Conservative 71; Mismatches 132; Indels 74; Gaps 16;	628 DDEKEANDDEEGDPSKRRRVENSIPAAGETONVEVAAGPAGKCAAVDVE :
KRARAEKKA : KPAOKKA	OY 677 PPSKQKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSMQEPDTKLRPLFEACGEVVQ 734 :
QY 621 EKRGADEDDEKEMGDDEEEQPSKRRRVENSIPAAGETQNVEVAAGPAGKCAAVDVEPPSK 680 : :	735 IRPIFSNRGDFRGYCYVEFKEEKSALQALEMDRKSVEGRPMFVSPCVDKSKN-PDFKVFR
QY 681 QKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSMQEPDTKLRPLFEACGEVVQIRPIFS 740 ::	Qy 794 YSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRL-VTN 835
QY 741 NRGDFRGYCYVEFKEEKSALQALEMDRKSVEGRPMFVSPCVDKSKNPDFKVFRYSTSL 798	Qy 836 RAGKPKGLAYVEYENESQASQAVMKMDGMTIKENIIKV 873
QY 799EKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTNR-AGKPKGLAY 845 S91 FRSGDGGDEKKIFVKGFDASLSEDDIKNTLREHFSSCGEIKNVSVPIDRDTGNSKGIAY 450	RESULT 14 A40252 elav protein - fruit fly (Drosophila virilis)
QY 846 VEYENESQASQAVMKMDGMTIKENIIKVAISNPPQRKVPEKPETRKAPGGPMLLPQTYGA 905 1	pecies: Drosophila ate: 06-Dec-1991 # ccession: A40252 ao, K.M.; White, F
Qy 906 RGKGR 910 Db 493 RGNGR 497	Mol. Cell. Biol. 11, 2994-3000, 1991 A.Fitle: Organizational analysis of elav gene and functional analysis of ELAV protein A.Reference number: A40252; MUID:91246165; PMID:1903840 A.Accession: A40252
RESULT 13 T17297	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-521 <yao></yao>
hypothetical protein DKFZp586F1023.1 - human C.Species: Homo sapiens (man) C.Species: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 31-Jan-2000	A; Gene: FlyBase:Dvir/elav A; Cross-references: FlyBase:FBgn0013110 C; Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleopro
R.Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999 A.Reference number: 218729	F;10-100/keglod: glutamine/alamine-fich F;180-268/Domain: ribonucleoprotein repeat homology <rrm1> F;287-355/Domain: ribonucleoprotein repeat homology <rrm2> F;441-508/Domain: ribonucleoprotein repeat homology <rrm3></rrm3></rrm2></rrm1>
A.Status: preliminary A.Molecule type: mRNA A.Residues: 1-960 (AANS> A.Residues: 1-960 (AANS>	Query Match Best Local Similarity 19.5%; Pred. No. 8.7e-05; Matches 89; Conservative 102; Mismatches 154; Indels 111; Gaps 17;
	QY 552 MERTEGSLEDWDIAVQKTETRLARVNEQRMKAABEKEAALVQQEEEKAEQRK 602 ::::::::::::::::::::::::::::::::::::
C, Supertamini); unassigned fibonucleoprotein repeat-containing proteins; ribonucleoprotein Query Match Query Match Best Local Similarity 22.4%; Pred. No. 4e-05; Matches 116; Conservative 80; Mismatches 173; Indels 149; Gaps 22;	QY 603 RARAEKKALKKKKIRGPEKRGADEDDEKEWGDDEEEQPSKRRRVENSIPAAGETQ 658 : : : : : : : : : :
ATDY-VEIWQAYLDYLRRRVDFKQDSSKELEELRA 4 :	Qy 659 NVEVAAGPAGKCAAVDVEPPSKQKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSMQEP 718 1
	QY 719 DTKLRPLFEACGEVVQIRPIFSNRGDFRGYCYVEFKEEKSALQA 762 : : : : :
508 ANMWLEYYNLERAHGDTQHCRKALH	QY 763LEMDRKSVEGRPMFVSPCVDKSKNPDFKVFRYSTSLEKHKLFISGLPFSCTKEELE 818 : : : : : :

qa	260 VLNGLRLQNKTIKVSFARPSSDAIKGÄNLYVSGLPKTMTQQELE 303		Db 419 IR-LVSQDGKSKGIAYIEFKSEADAEKNLEEKQGAEIDGRSVSLYYTGEKGQRQERTGKN 477
oy Dp	819 EICKAHGTVKDLRLVINRAGKPKGLAYVEYENESQASQAVMKMDGMIKENIIKVA 874 : : : : : : : 304 AIFAPFGAIITSRILQNAGNDTQTKGVGFIRFDKREEATRAIIALNGTTPSSCTDPIVVK 363	•	OY 794 YSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTNRAGKPKGLAYVEYENESQ 853 :
oy Og	LDVML		**************************************
Qy			arch completed: June 18, 2003, 13:52:14 b time : 30 secs
RESULT 15 A2741 nucleolin N; Alterna C; Species C; Date: 1 C; Access R; Lapeyre A; Title: A; Referen A; Referen A; Referen A; Residue A; Residue A; Referen A; Referen A; Residue A; Referen A; Referen A; Residue A; Residue A; Referen A; Referen A; Residue A; Residue A; Residue A; Referen A; Referen A; Residue A; Residue A; Residue A; Residue A; Referen A; Refere	RESULT 15 A27441 nucleolin - Chinese hamster Nalternate names: nonchromosomal protein C23; nucleolar protein C23 (Species Cafcetulus grissus (chinese hamster) C; Species (Includius grissus (chinese hamster) C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999 R; Lapeyre, B.; Bourbon, H.; Amalric, F. Proc. Natl. Acad. Sci. U.S.A. 44, 1472-1476, 1987 A; Telepeyre Natl. Amalric, F. A; Molecule type: mRN A; Residues: 1-713 < (LAP) A; Residues: 52-541, G7, 543-544, 7R', 546-713 < (LAZ) A; Residues: 52-541, G7', 543-544, 7R', 546-713 < (LAZ) A; Residues: 52-541, G7', 543-544, 7R', 546-713 < (LAZ) A; Residues: 52-541, G7', 543-544, 7R', 546-713 < (LAZ) A; Residues: 52-541, G7', 543-544, 7R', 546-713 < (LAZ) A; Residues: 52-541, G7', 543-544, 7R', 546-713 < (LAZ) A; Residues: 52-541, G7', 543-544, 7R', 78 & (LAZ) A; Residues: 52-541, G7', 543-544, 7R', 78 & (LAZ) A; Residues: 52-541, G7', 543-544, 7R', 78 & (LAZ) A; Residues: 52-541, G7', 543-544, 7R', 78 & (LAZ) A; Residues: 52-541, G7', 543-544, 7R', 78 & (LAZ) A; Residues: 52-541, G7', 543-544, 7R', 78 & (LAZ) A; Residues: 52-541, G7', 543-544, 7R', 78 & (LAZ) A; Residues: 10ning of cDNA encoding a 100 kDa nucleolar protein (nucleoline) of Chinese ha A; Residues: 179-218 & (LAZ) A; Residues: 170-170; Residues: 170-170; Residues: 170-170; Residues: 170-170; Residues:		
Query M Best Lo Matches			
Oy Dp	583 AAEKEAALVQQEEEKAEQRKRARAEKKALKKKKIRGPEKRGA 		
Qy Dp	631 KEWGDDEEEQ 661 : : : 246 EEDEDEEEEDEEEEEEEEEEEEEVKPAPGKRKKEWTKQKEVPEA-KKQKVEGSEST 304		
Qy	662EKAA 686 :		
Oy GD	687 SLKRDMPKVLHDSSKDSITVFVSNLPYSMQEPDTKLRPLFEACGEVVQ 734		
0y	735 IRPIFSNRGDFRGYCYVEFKEEKSALQALEMDR-KSVEGRPMFVSPCVDKSKNPDFKVFR 793		

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OM protein - protein search, using sw model

June 18, 2003, 13:46:53; Search time 15 Seconds (without alignments) 2662.780 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-763-985A-2 4994 1 MATAAETSASEPEAESKAGP......AATEAPKMSNADFAKLFLRK 963

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P20397 xenopus lae	P27476 saccharomyc	drosop	gallu	homo sa	mus m	homod	drosc		P13383 rattus norv	Q9ukx3 homo sapien	mus m	Q11102 caenorhabdi				P90978 caenorhabdi				•	_	P26369 mus musculu	P13535 homo sapien		-	P13539 mesocricetu	P90727 caenorhabdi		9	~	7312	P13540 mesocricetu
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	192.5	191.5	191	190.5	189	189	188.5	188	187.5	187.5	187.5	187	
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ALIGNMENTS

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"The NSRI gene encodes a protein that specifically binds nuclear localization sequences and has two RNA recognition motifs.";
J. Cell Biol. 113:1-12(1991).
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P -> Q (IN REF. 2).
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D -> E (IN REF. 2).
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ARG/GLY/PHE-RICH.
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01-AUG-1992 (Rel. 23, Last sequence update)
16-CGT-2001 (Rel. 40, Last annotation update)
Nuclear Jocalization sequence binding protein (P67).
NSR1 OR YGR159C OR G7001.
Saccharomyces cerevisiae (Baker's yeast)
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                                    ASP/GLU-RICH (ACIDIC)
ASP/GLU-RICH (ACIDIC)
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26.5%; Pred. No. 3e-09;
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PE -> LR (IN RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                **NOCETOR INVOLVED IN PRE-RRNA PROCESSING. SPECIFICALLY BINDS INCLEAR LOCALIZATION SEQUENCES. CANDIDATE FOR A RECEPTOR AT THE NUCLEUS THAT MAY BE INVOLVED IN BOTH RNA AND PROTEIN TRANSPORT. BINDS TELOMERIC SEQUENCES OF THE TYPE (TG[1-3])N IN VITRO. SUBCELLULAR LOCATION: NUCLEAR; POSSIBLY AT THE NUCLEOLUS. IN RESPONSE TO LOW TREMERATURE (BY COLD-SHOCK). IN RESPONSE TO LOW TREMERATURE (BY COLD-SHOCK). IS IMILARITY: BELONGS TO THE GAR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A39205; A39205.
SGD; S000391, NSR1.
InterPro; IPP00076; rrm; 2.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
PROSITE; PS50036; RRM; 2.
DNA-binding; RNA-binding; Nuclear protein; Repeat; rRNA processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that encode proteins that bind to (TG1-3)n single strand telomeric DNA in vitro.";
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RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
RNA-BINDING RRM) 2.
RNA-BINDING RGG-BOX (BY SIMILARITY).
90DEEF7BBC20BCOC CRC64;
                                                                                                                                                                                                                             "The sequence of a 27 kb segment on the right arm of chromosome from Saccharomyces cerevisiae reveals MOLL, NAT2, RPL30B, RSRL, PEMI/CHO2, NSRI genes and ten new open reading frames."; Yeast 11:1421-1427(1995).
                                                                similarity to mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rieger M., Mueller-Auer S., Brueckner M., Schaefer M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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(2.2%; Pred. No. 9.5e-08;
ve 84; Mismatches 172;
                                                      "Yeast NSRI protein that has structural similar
nucleolin is involved in pre-rRNA processing.";
J. Biol. Chem. 267:16252-16258(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 22:4906-4913(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin J.-J., Zakian V.A.;
"Isolation and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95098604; PubMed=7800479;
MEDLINE=92355583; PubMed=1644811;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z72946; CAA97180.1; -.
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Best Local Similarity 22.2
Matches 84; Conservative
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345
                                   Inouye M.;
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Amanatides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Hilp W., Hoskins R.A., Galle R.F.,
A Adams M.D., Celliker S.E., Hilp W., Hoskins R.A., Galle R.F.,
A Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthman J.H., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazel F.G., Change M., Pfeliffer B.D.,
An K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Buck J., Brandari D., Bolshakov S.,
Ballew R.M., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Borkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
Borkova D., Botchan M.R., Dunke C., Davenport L.B., Davies P.,
Borkova D., Botchar M.R., Dong Z., Mays A.D., Daw I., Dlatz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunk P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunk P.,
RA Glodek A., Gong F., Gorrell J.H., Re Z., Rennison J.A., Harris M.,
Harris N.L., Harvey D., Heinan T.J., Wein M.-H., Ibegwam C.,
Alalali M., Kalush F., Karpen G.H., Ke Z., Kanitson J.A.,
Alalali M., Kalush F., Karpen G.H., Ke Z., Kanitson D.,
Alaktei B.L., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Alaktei B.L., McIntcosh T.C., McLeod M.P., Mocherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy U., Marny D.M., Nelson D.E.,
                                                                                                                                                                                               QNVEVAAGPAGKCAAVDVEPPSKQKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSMQE 717
                                                                                                                                                      718 PDTKLRPLFEACGEVVQIRPIFSNRGD-FRGYCYVEFKEEKSALQAL-EMDRKSVEGRPM 775
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                                                                                                                                                                                                                                                                                                                                                                                       240 NCDMSTSKPAGNNDRAKKFGDTPSEPSDTLFLGNLSFNADRDALFELFAKHGEVVSVRIP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    834 TN-RAGKPKGLAYVEYENESQASQAVMKMDGMTIKENIIKVAISNPPQRKVPEKPETRKA 892
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300 THPETEQPKGFGYVQFSNMEDAKKALDALQGEYIDNRPYRLDFSSP------RPNNDGG 352
                                                P17886; Q24283; O46071;
P17886; Q24283; O46071;
D1-WAR-1992 (Rel. 21, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
CCRON OR EG:3088.1 OR CG3193.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.
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"The crooked neck gene of Drosophila contains a motif.found in a family of yeast cell cycle genes.";
Genes Dev. 5:1080-1091(1991).
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MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- DEVELOPMENTAL STAGE: IS EXPRESSED THROUGHOUT EMBRYONIC, LARVAL, PUPAL AND ADULT STAGES AT RELATIVELY CONSTANT LEVELS.
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reincrt K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i - FUNCTION: INVOLVED IN NEUROGENESIS. LOSS OF ZYGOTIC EXPRESSION OF CRN CAUSES DEFECTS IN THE PROLIFERATION OF BRAIN NEUROBLASTS AND RESULTS IN THE ABSENCE OF IDENTIFIED NEURONAL LINEAGES IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.

-i - SUBCELLULAR LOCATION: NUCLEAR (POSSIBLE).

-i - TISSUE SPECIFICITY: TRANSCRIBED IN ALL CELLS DURING EMBRYONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAT 12.
HAT 13.
HOCLEAR LOCALIZATION SIGNAL (POTENTIAL).
R -> P (IN REF. 1).
                                                                                                                                                                                                                                  MEDLINE-2019601; PubMed=10731137;
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
Breano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden Kiamos I., Bolshakov S.,
Rapagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Beinert N., Dowe G., Schoettler P., Werner M., Mourkioti F.,
Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
Glover D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                              "From sequence to chromosome: the tip of the X chromosome of D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.0.0.00
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EMBL; AE003423; AAF45760.1; -.
EMBL; AL009195; CAA15705.1; -.
PIR; A39654; A39634.
                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster.";
Science 287:2220-2222(2000)
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InterPro; IPR001440; TPR.
Pfam; PF02184; HAT; 10.
SMART; SM00386; HAT; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein; Repeat;
REPEAT 56 88
REPEAT 90 122
REPEAT 124 156
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1124
1128
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583 AAEKEAALV-----
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Best Local Similarity 22.0
Matches 94; Conservative
 SEQUENCE FROM N.A.
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                                                                                                                                               LEGELTKVRMARQKMSEIFPLTEELWLEWLHDE-----ISMAQDGLDREHVYDLFEK 175
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NUCL_CHICK STANDARD; PRT; 694 AA.

NUCL_CHICK
P15771.

101-APR-1990 (Rel. 14, Last sequence update)

101-APR-1990 (Rel. 41, Last annotation update)

101-JMN-2002 (Rel. 41, Last annotation update)

Nucleolin (Protein C23).

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

Gallus.

NCBI_TAXID-9031;
                                           Gaps
                                         Conservative 115; Mismatches 259; Indels 213;
                    Length 702;
 8E03A869B84E4A12 CRC64;
                    DB 1;
                   Score 268.5; DB 7
                                                                                                      E--YDEEEEKNQL-----EIERLEEQLS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- ETQNVEVAAGPAGKCAAVDVEP 677
 84261 MW;
                    5.4%;
702 AA;
                               Best Local Similarity
Matches 157; Conserv
SEQUENCE
                    Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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ARG/GLY/PHE-RICH.
5 X 7 AA TANDEM REPEATS OF X-T-P-X-K-K-X.
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PROSITE; PS00030; RRM_RNP_1; 3.
Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat;
                                                                                                                                                                                                                                                                                                                          coordinate expression of two abundant non-ribosomal nucleolar
                                                                                                                                                                                                                                                                                                                                                                                                           5SQUENCE OF 407-694 FROM N.A.
SEQUENCE OF 407-694 FROM N.A.
BEDINE-89119560; PubMed-2914325;
BOTER R.A., Lehner C.F., Eppenberger H.M., Nigg E.A.;
BOTER R.A., Lehner C.F., Eppenberger H.M., Nigg E.A.;
Major nucleolar proteins shuttle between nucleus and cytoplasm.";
"Major nucleolar proteins shuttle between profess and cytoplasm.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLEGLAR CHROMATIN AND PRERIBOSOMAL PARTICLES. IT INDUCES CHROMATIN DECONDENSATION BY BINDING TO HISTOME H1. IT IS THOUGHT TO PLAY ROLE IN PRE-RRNA TRANSCIPTION AND RIBOSOME ASSEMBLY.
-!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
-!- SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).
                                                   J E.A.; of chicken nucleolin/C23 and NO38/B23, two major
                                                                                                                                                                                                                         MEDLINE-90304215; PubMed-2114180;
Maridor G., Krek W., Nigg E.A.;
"Structure and developmental expression of chicken nucleolin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
SIMILARITY).
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A -> R (IN REF. 3).
N -> T (IN REF. 3).
7996C504BE9459A1 CRC64;
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ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
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                                                                                                                              Nucleic Acids Res. 18:1286-1286(1990)
      PubMed=2320420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000504; RNA_rec_mot.
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75640 MW;
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                                                                                                                                                                                            DISCUSSION OF SEQUENCE.
MEDLINE=90206792; Pub
Maridor G., Nigg E.A.
"CDNA sequences of ch
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HSSP; P09651; 1UP1.
                                                                                                    nucleolar proteins."
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11; 609

Gaps

Indels 118;

66; Mismatches 149;

6.4e-07

---QQEEEKAEQRKRARAEK--

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14;
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ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
RNA-BINNING (RRM) 1.
RNA-BINNING (RRM) 3.
RNA-BINNING (RRM) 4.
ARG/GLY/PHE-RICH.
8 X 8 AA TANDEM REPEATS OF X-T-P-X-K-K-X-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|||:|
266 EEEEEPVKEAPGKRKKEMAKQKAAPEAKKQKVEGTEPTTAFNLFVGNLNFNKSAPELKTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----AAGETQNVEVAAGPAGKCAAVDVEPPSKQKEKAASL------KRDMPKVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- DEKEWGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 EEEAMETTPAKGKKAAKVVPVKAKNVAEDEDEEEEDDEDDDDDDDDDDDDDDDDDEDDEEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSSK - - DSITVFVSNLPYSMQEPDTKLRPLFEACGEVVQIRPIFSNRGDFRGYCYVEFKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEELEEICKAHGTVKDLRLVTNRAGKPKGLAYVEYENESQASQAVMKMDGMTIKENIIKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             636 DEEEOP------SKRRRVENSIP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKSALQALEMDR-KSVEGRPMFVSPCVDKSKNPDFKVFRYST-SLEKHKLFISGLPFSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                            Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat; RNA-binding.

INIT_MET

DOMAIN

142

170

ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97;
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PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
85AZFZCAZZEAO3DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 245.5; DB 1;
Pred. No. 5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            595 EEKAEQRKRARAEKKA----LKKKKKIRGPEKRGADED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INCOMPLETE)
                                               HSSP; P09651; 1HA1.
Aarhus/Ghent-2DPAGE; 1210; NEPHGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   874 AISNPPQRKVPEKPETRKAP 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   555 ELQGP----RGSPNARSQP 569
                                                                                                              InterPro; IPR000504; RNA_rec_mot
Pfam; PF00076; rrm; 4.
SMART; SM00360; RRM; 4.
                                                                                                                                                              PROSITE; PS50102; RRM; 4.
PROSITE; PS00030; RRM_RNP_1; 3.
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126
134
144
152
183
76213 MW;
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EMBL; M60858; AAA59954.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                      64
81
89
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103
                                                                              HGNC:7667; NCL.
                 A35804; A35804.
S04631; S04631.
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152
183
706 AA;
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1184
233
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392
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571
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15;

Gaps

66;

Indels

Length 706;

299

727

us-09-763-985a-2.rsp

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728 ACGEVVQIRPIFSNRGDFRGYCYVEFKEEKSALQALEMDR-KSVEGRPMFVSPCVDKSKN 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 EGSEPTTPFNLFIGNLNPNKSVNELKFAISELFAKNDLAVVDVRTGTNRKFGYVDFE-SA 358
                                                                                                                                                                                                                                                               553 ERTEGSLEDWDIAVQKTETRLARVNEQRMKAAEKEAALVQQEEEKAEQRKRARAEKKALK
                                                                                                                                                                                                                                                                                200 EEDDDEEEEDDSEEEVMEITTAKGKKTPAKVVPMKAKSVAEEEDDEEE-----
                                                                                                                                                                                                                                                                                                                                       248 ------DEDDEDDEEEDDEDDEEEEEEPVKAAPGKRKKEMTKQKEAPEAKKQKV
                                                                                                                                                                                                                                                                                                                                                                                    648 ENSIP------AAGETQNVEVAAGPAGKCAAVDVEPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                              680 KOKEKAASL-----KRDMPKVLHDSSK--DSITVFVSNLPYSMQEPDTKLRPLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              787 PDFKVFRYST-SLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTNRAGKPKGLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       613 KKKKIRGPEKRGADEDDEKEWGDD----EEEQP-----SKRRRV
PHOSPHORYLATION (BY SIMILARITY). 8 X 8 AA TANDEM REPEATS OF X-T-P-X-K-K-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain;
MEDILINE-994003880; PubMed-9734811;
Ishlikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                   89505EE39C89F832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 846 VEYENESQASQAVMKMDGMTIKENIIKVAISNPPQRKVPEK 886
                                                                                                                                                                                                 4.9%; Score 244.5; DB 1;
24.7%; Pred. No. 5.7e-06;
ive 65; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               097478; 090FN5;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable RNA-binding protein KIAA0682.
                                                                                                        (INCOMPLETE)
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                                                                                                                                                                   76592 MW;
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Best Local Similarity 24./.,
Conservative
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706 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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REPEAT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                       **MEDLINE-91317840; PubMed-1860869; MEDLINE-91317840; PubMed-1860869; MEDLINE-91317840; PubMed-1860869; MEDLINE-91317840; PubMed-1860869; MEDLINE-91317840; Dinding to target cell proteins. Granzyme A binding to target cell proteins. Granzyme A binds to and cleaves nucleolin in vitro."; cleaves nucleolin in vitro."; L. J. Biol. Chem. 266:14708 (1991).

1. J. Biol. Chem. 266:14703 14708 (1991).

1. SUNCTION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTEIN OF GROWING CHARAYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANCCIEDLAR CHARAYOTIN AND PRERIBOSOMAL PARTICLES. IT INDUCES CHROMATIN DECONDENSATION BY BINDING TO HISTORE H.]. IT IS THOUGHT TO PLAY A ROLE IN PRE-RRNA TRANSCEIPTION AND RIBOSOME ASSEMBLY.

2. SUNCELLULAR LOCATION: Nuclear; nucleolar.

2. SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                                               reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50102; RRM; 4.
PROSITE; PS00030; RRM_RNP_1; 3.
Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat;
RNA-binding.
                                                                                                                                                                                                                                                           The complete sequence reverby two independent exons."
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAN-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 4.
ARG/GLY/PHE-RICH.
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-44 FROM N.A.
MEDLINE-89121496; PubMed-2906027;
BOUTDON H.M., Prudhomme M., Amalric F.;
Sequence and structure of the nucleolin promoter in rodents:
characterization of a strikingly conserved CpG island.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
           NUCL_MOUSE STANDARD; PRT; 706 AA. P09405; Q61991; 01-MAR-1989 (Rel. 10, Created) 10-MAR-1989 (Rel. 10, Last sequence update) 10-JUN-2002 (Rel. 41, Last annotation update) Nucleolin (Protein C23).
                                                                                                                                                                                                      STRAIN-BALB/C;
STRAIN-BALB/C;
MEDLINE-88316930; PubMed-3137346;
Bourbon H., Lapeyre B., Amalric F.;
Structure of the mouse nucleolin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P09651; 1HA1.
MGD; MGI:97286; Ncl.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 4.
SWART; SM00360; RRM; 4.
                                                                                                                                                                                                                                                                        that each RNA binding domain is J. Mol. Biol. 200:627-638(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X07699; CAA30538.1; -. EMBL; M22089; AAA39841.1; -.
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467
560
643
696
156
                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                               Gene 68:73-84(1988).
                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                    NCBI_TaxID=10090;
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1189
240
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MOD_RES
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InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 3.
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HSSP; P19339; 2SXL.
FlyBase; FBgn0013110; Dv1r\elav.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila virilis (Fruit fly).
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PROSITE; PS00030; RRM_RNP_1;
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                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
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                    Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D. Wambutt R., Korn B., Klein M., Poustka A.;

"Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";
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Gassenhuber J., Glassl
auersachs S., Blum H.,
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1D457D54B3D95377 CRC64;
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-!- SIMILARITY: CONTAINS 6 RNA RECOGNITION MOTIFS (RRM)
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SWISS-2DPAGE; 0974C8; HUMAN.
INTERPO: IPR000504; RNA_rec_mot.
Pfam: PF00076; rrm; 6.
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PROSITE; PS00030; RRM_RNP_1;
RNA-binding; Repeat.
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960 AA;
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                                                                                                   603 RARAEKKALKKKKK---IRGPEKRGADEDDEKEWGDDEEEQPSKRRRVENSIPAAGETQN 659
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Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elay protein (Embryonic lethal abnormal visual protein).
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                                                                                                                                                                                                         Conservative 103; Mismatches 154;
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110 QQVVQQQQVQQAVQAVQQQQQQQQQQQQQQQQVVQQQQQVVQQQVQQQVTNGN	660 VEVAAGPAGKCAAVDVEPPSKQKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSNGEPD : : : : : : : : : :	720 TKLRPLFEACGEVVQIR	763LEMDRKSVEGRPMFVSPCVDKSKNPDFKVFRYSTSLEKHKLFISGLPFSCTKEELEE	820 ICKAHGTVKDLRLVTNRAGKPKGLAYVEYENESQASQAVMKMDGWIKENIIKVAI 1	876 SNPPQRKVPEKPETRKAPGGPMLLPQTYGARGKGRTQLSLLP	918 RALGRPSAAAPQAENGPAAAPAVAAPAATEA 948 1	RESULT 9 NUCL_MESAU STANDARD; PRT; 713 AA.	P08199; 01-AUG-1988 (Rel. 08, Created) 01-AUG-1988 (Rel. 08, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Mucleolin (Protein C23).	Mesocricetus auratus (Golden hamster). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi. Mammallai Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus. NCBL_TaxID=10036;	11) SEQUENCE OF 35-713 FROM N.A., AND SEQUENCE OF 1-34. BEDLINE-87175501; Pubmed-3470736;	Mucleolin, the major nucleolar protein of growing eukaryotic cells an unusual protein structure revealed by the nucleotide sequence."; Proc. Natl. Acad. Sci. U.S.A. 84:1472-1476(1987).	FUNCTION FUNCTION MEDLINE-88312631; PubMed-3409881; Erard M.S., Belenguer P., Caizergues-Ferrer M., Pantaloni A	Amalure rucleolar protein, nucleolin, induces chromatin decondensation by binding to histone H1.";	EUI. J. BLOCHEM. 1/0:325-33U(1988)1- FUNCTION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTEIN OF GROWING EUKARKOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLEDLAR CHROMATIN AND PRERIBOSOMAL PARTICLES. IT INDUCES CHROMATIN	DECONDENSATION BY BINDING TO HISTONE H1. IT IS THOUGHT TO PLAY ROLE IN PRE-FREN TRANSCRIPTION AND RIBOSOME ASSEMBLY!- SUBCELLULAR LOCATION: Nuclear; nuclealar!- SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).	his SWISS-PROT entry is copyright. It is produced through	between the Swiss institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

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EEDEEEEEEDEEEEEEEEEEPVKPAPGKRKKEMIKQKEVPEA-KKQKVEGSESI 304
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                                                                                                                                                                                                                                                                           4.5%; Score 224.5; DB 1; Length 713;
ity 23.5%; Pred. No. 6.7e-05;
servative 67; Mismatches 134; Indels 105; Gaps
                                                                                                     12; RRM; 4.
10; RRM_RNP_1; 3.
1; Phosphorylation; Methylation; DNA-binding; Repeat;
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PHOSPHORYLATION.
PHOSPHORYLATION.
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0504; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 4.
ARG/GLIY/PHB-RICH.
8 X 8 AA TANDEM REPEATS OF X-T-P-X-K-K-X-X.
                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                              Bourbon H.-M., Amalric F.;
"Nucleolin gene organization in rodents: highly conserved sequences
within three of the 13 introns.";
Gene 88:187-196(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50102; RRM; 4.
NOSSTE; PS00030; RRM_RNP_1; 3.
Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat;
RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                   EURARYOTIC CELLS. IT IS FOUND ASSOCIATED WITH INTRANUCLEDLAR CHROMATIN AND PRERIBOSOMAL PARTICLES. IT INDUCES CHROMATIN DECOMDENSATION BY BINDING TO HISTONE HI. IT IS THOUGHT TO PLAY ROLE IN PRE-RRNA TRANSCRIPTION AND RIBOSOME ASSEMBLY. SUBCELLULAR LOCATION: Nuclear; nucleolar. SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIES (RRW).
                                                                                                                                                                                                                                                                                                                                                     characterization of a strikingly conserved CpG island.";
Gene 68:73-84(1988).
-!- FUNCTION: NUCLEOLIN IS THE MAJOR NUCLEOLAR PROTEIN OF GROWING
                                                                                                                                                                                                                                                                                                                                            promoter in rodents:
854 ASQAVMKMDGMTIKENIIKVAISNPPQRKVPEKPETRKAP 893
                    AKEALNSCNKMEIEGRTIRLELQGP-----RGSPNARSQP
                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-LUN-2002 (Rel. 41, Last annotation update)
Nucleolin (Protein C23).
                                                                                712 AA
                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-44 FROM N.A. MEDLINE-89121496; PubMed=2906027; BOLLFOD H.-M., Prudhomme M. Amalric F.; Sequence and structure of the nucleolin
                                                                               PRT;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=90269607; PubMed=2347493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M55015; AAA41732.1; JOINED.
EMBL; M55017; AAA41732.1; JOINED.
EMBL; M55020; AAA41732.1; JOINED.
EMBL; M22090; AAA41733.1; -.
PIR; JH0148; JH0148.
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InterPro.; PPR000504; RNA_rec_mot.
Pfan: PPF00076; rrm; 4.
SMART; SM00360; RRM; 4.
                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
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                                                                                STANDARD;
                                                                                                                                                                Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420 VEIR-LVSQDGRSKGIAYIEFKSEADAEKNLEEKQGAEIDGRSVSLYYTGEKGQRQERTG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         479 KNSTWSGESKTLVLSNLSYSATEETLQEVFEKATFIK---VPQNPHGKSKGYAFIEFASF 535
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MEDLINE=99318869; PubMed=10388558;
Weiss A., Schiaffino S., Leinwand L.A.;
"Comparative sequence analysis of the complete human sarcomeric myosin heavy chain family: implications for functional diversity.";
J. Mol. Biol. 290:61-75(1999).
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"The human extraocular muscle myosin heavy chain gene (MYH13) maps to
the cluster of fast and developmental myosin genes on chromosome 17.";
Genomics 54:188-189(1998).
-i- FUNCTION: MUSCLE CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AASL------KRDMPKVLHDSSK--DSITVFVSNLPYSMQEPDTKLRPLFEACGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             792 FRYSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTNRAGKPKGLAYVEYENE
                                                                                                                                                                                                                                                                                                                                               553 ERTEGSLEDWDIAVQKTETRLARVNEQRMKAAEKEAALVQQEEEKAEQRKRARAEKKALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                613 KKKKIRGPEKRGADEDDEKEWGDDEEEQP-----SKRRVENSIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------AAGETQNVEVAAGPAGKCAAVDVEPPSKQKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 TTPFNLFIGNLNPNKSVAELKVAISELFAKNDLAAVDVRTGTNRKFGYVDFE-SAEDLEK
                                                                                                                                                                                                                                                                                                                                                                                             EEDDSEEEVMEITPAKGKKTPAKVVPVKAKSVAEE----EEDDEDDEDEEEDEDEE----
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                              98;
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16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, skeletal muscle, extraocular (MyHC-eo)
                                                                                                                                                                                                                                             Length 712;
                                                                                                                                                                                                                                                                                              72; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         536 EDAKEALNSCNKMEIEGRTIRLELOGP----RGSPNARSOP 572
                                                                                                                                                                                             68774A214E550F90 CRC64;
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                                                                                                                                                                                                                           Score 224; DB 1,
No. 7.1e-05;
                                                                                                 (INCOMPLETE)
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MEDLINE-99026150; PubMed-9806854;
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16-0CT-2001 (Rel. 40, Last sequ
16-0CT-2001 (Rel. 40, Last anno
                                                                                                                                                                                               77016 MW;
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64
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89
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1103
126
                                                                                                                                                                                             712 AA;
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57
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Q9UKX3; 095252;
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1126 IEAEHTL-----RAKIEKQRSDLARELEEISERLEEASGATSAQIEMNKK--REAEFQKM 1178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1569 LSQVK-----SELDRKVIEKDEE-IEQLKRNSQRAAEALQSVLDAEIRSRNDALRLKKK 1621
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                                                                                                                            ----RRDLEEATLQHEATAATLRKKQADSVAELGEQIDNLQRVKQKLEKEKSELKMEIDD 1234
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                                                                                                                                                                                                                                                                              335 -RALVENCLVPDLWIRYSQYLDRQLKVKDLVLSVHNRAIRNCPWTVALWSRYLLAMERHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     534 AVQCTSDYPEHVCE------VLLTMERTEGSLEDWDIAVQKTETR
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                              301 ALLQAEAPRLAEYQAYID-----FEMKIGDPARIQLIFE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYHB_MOUSE STANDARD; PRT; 1972 AA. 008638; 008639; Q65462; Q64195; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Myosin heavy chain, smooth muscle isoform (SMMHC). MYH11.
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SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) SUBURITS (MLC) 2 SUBCELLULAR LOCATION: Thick filaments of the myofibrils. DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMMOSED OF 4 HEPTAPEFTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY. MISCELLANGOUS: EACH WYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROWYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.4%; Score 220.5; DB 1; Length 1938;
19.5%; Pred. No. 0.00041;
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130 METHYLATION (TRI.) (POTENTIAL).
699 ALKYLATION (SH-1) (POTENTIAL).
709 ALKYLATION (SH-2) (POTENTIAL).
223678 MW; 1F6D006416381CD5 CRC64;
                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
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ATP (POTENTIAL).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
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InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
Pfam; Pr00063; myosin_head.
Pfam; Pr00612; IQ; 2.
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ProDom; PD000355; myosin_head; 1.
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SMART; SM00242; MYSc; I.
PROSITE; PS50096; IQ; I.
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130 13:
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1938 AA;
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                                                                                                                                                                                                                                                                                                                                            A SUZUKI T., Kim H.S., Kurabayashi M., Hamada H., Fujii H., Aikawa M., Watanabe M., Sakomura Y., Yazaki Y., Nagai R.; Awatanabe M., Sakomura Y., Yazaki Y., Nagai R.; Matanabe M., Sakonoth muscle cells. Use of retinoic acid and antisense against the central nervous system-specific Pou transcription factor Brn-2."; Circ. Res. 78:395-404(1996).

1. Circ. Res. 78:395-404(1996).

2. I- SUBUNIT: MUSCLE CONTRACTION.

2. SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC).

3. SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

4. ALTERNATIVE PRODUCTE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING PRODUCED BY ALTERNATIVE SPLICING.

5. I- ALTERNATIVE PRODUCTE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

6. I- PUM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

6. I- PUM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY MENOMYOSIN (LMM) AND 1 HEAVY MENOMYOSIN (HMM). IT CAN LAFER BE SELECTIVELY PREDENDARME SET OF 2 SELECTION (LMM) AND 1 HEAVY MENOMYOSIN (HMM). IT CAN LAFER BE SELECTION (LMM) AND 1 HEAVY MENOMYOSIN (HMM). IT CONDUCTED STRUET PROTEINS (S1) AND 1 ROD-SHARED CHEREDARMENT (S1) AND 1 ROD-SHARED
                                STRAIN=BALB/c; TISSUE-Uterus; MEDILINE=97242182; PubMed=9125171; Hasegawa K., Arakawa E., Oda S., Matsuda Y.; Molecular cloning and expression of murine smooth muscle myosin heavy
                                                                                                                                                                                                            Mdano J.M., Cserjest P., Ligon K.L., Periasamy M., Olson E.N.; "Smooth "uscle myosin heavy chain exclusively marks the smooth muscle lineage during mouse embryogenesis."; Circ. Res. 75:803-812(1994).
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SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 1Q DOMAIN.
                                                                                                                      Biochem. Biophys. Res. Commun. 232:313-316(1997)
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Pfam; PF02736; Myosin_N; 1.
PRINES; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                            MEDLINE=95008063; PubMed=7923625;
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InterPro; IPR001609; myosin_head
'fam; PF00063; myosin_head; 1.
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InterPro; IPR004009; Myosin_N.
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                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-126 FROM N.A.
                                                                                                                                                       SEQUENCE OF 1-368 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1476 AEAREKETKALSLARALEEALEAKEELERTNKMLKAEMEDLVSSKDDVGKNVHELEKSKR 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1060 LEGDASDFH-----EQIADLOAQIAELKMOLAKKEEELQAALARLDEEIAQKNNALKKIR 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKLEVQLQDLQSKCSDGERARAELSDKVHKLQNEVESVTGMLNEAEGKAIKLAKDVASLG 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERALSSVGLHMTKGLALWEAYREFESAIVEAARLEKVHSLFRRQLAIPLYDMEATFAEYE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K------CLVPDLWIRY 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 VTFEKALNAGFIQATDYVEIWQAYLDYLRRRVDFKQDSSKELEELRAAF-TRALEYLK-Q 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              505 AKYANMWLEYYNLERAHGDTQHCRKALHRA------VQCTSDYPEHVCEV---- 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 WLHDEISMAQDGLDREH-VYDLFEKAVKDYICPNIWLEYGQYSVGGIGQKGGLEKVRSVF 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 EWSEDPIPESVIQ-----NYNKALQQLEKYKPYEEALLQAEAPRLAEYQAYIDFEM 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----EEGVSE-----SDGDEYA-----MASSAESSPGEYEWEYDEEEEEKNQLEIERLEEQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSINVYDYNCHVDLIRLLRLEGELTKVRMARQKMSE-----IFPLTEEL------WLE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         549 -LLT-MERTEGSLEDWDIAVQKTETRLAR--VNEQRMKA-------AEKEAALV 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --ALKKKKKIRGPEK 622
                                                                                                                                                                                                    METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
RGNESEVPSRAGGRRVIENTOCSEEMDARDSDFNGTKA
SE -> GPPPQETSQ (IN ISOFORM 2).
N -> D (IN REF. 3).
A -> V (IN REF. 2).
A -> K (IN REF. 2).
A -> K (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQYLDRQLKVKD-----LVLSVHNRAIRNCPWTVALWSRYLLAMERHGVDHQV-----IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 EPEAESKAGPKADGEE--DEVKAARTRRKVLSRAVAAATYKTMGP---AWDQQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 19.7%; Pred. No. 0.00061;
les 215; Conservative 169; Mismatches 384; Indels 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1972;
                                                                                                                                      ATP (POTENTIAL).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
  ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVEERFNESGDPSCVIMQNWARIEARLCNNWQKARELWDSIMT----
                                                                                        COILED COIL (POTENTIAL)
                                                                                                                   CARBOXYL-TERMINAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      592 QQ------EEEKAEQRKRARAEKK-------
                                               MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 217.5;
                       Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                            227026
                                                                                                                                                                                                                                                                                                                         126
161
189
                                                                                                                                                                                                                                                                                                                                                                                          1972 AA;
Calmodulin-binding;
                          Multigene family;
                                                                                                                                                                                                                                                                                                                                             161
189
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                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                DOMAIN
NP_BIND
DOMAIN
                                                                                                                                                                                                                                 MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                              /ARSPLIC
                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                              MOD_RES
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282 IQNYNKALQQLEKYKPYEEALLQAEAPRLAEYQAYIDFEMKIGDPARIQLIFERALV--- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "gar2 is a nucleolar protein from Schizosaccharomyces pombe required for 18S rRNA and 40S ribosomal subunit accumulation.";
Nucleic Acids Res. 23:1912-1918(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                     WDSIMT -- RGNAKYANMWLEYYNLERAHGDTQH -- -- -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                          500 AA
                                                                                                                                                                         DVT-----ALEKKLHNKEKEVQTLTKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95319932; PubMed-7596817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P41891; 013707;
01-NOY-1995 (Rel. 32, Created)
30-MAY-2000 (Rel. 39, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein gar2.
GAR2 OR SPAC140.02.
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VK 773
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GAR2_SCHPO
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                                                         1656 DFQRELDDARASRDEIFATSKENEKKAKSLEADLMQLQE----DLAAAERARKQA-DLEK 1710
                                                                                                                     1711 EELAEELASSLSG--RNTLQD-EKRRLEARIAQLEEELEEEQGNMEAMSDRVRKATLQAE 1767
                                                                                                                                                                                                                                                                                                  ||: :| :|| ::|
|1838 QAATKSLKQKDKKIKEVILQV----EDERKMAEQYKEQAE-------KGNTK 1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Burdean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                     QASQAVMKMDGWTIKENIIKVAISNPPQRKVPEKPETRKAPGGPMLLPQTYGARGKGRTQ 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYREFES-----AIVEAARLEKVHSL--FRRQLAIPLYDMEATFAEYEEWSEDPIPESV 281
                                                                                                                                                                         678 PSKQKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSMQEPDTKLRPLFEACGEVVQIRP
                              RGADEDDEKEWGDDE-----EEQPSKRRRVENSIPAAGETQNVEVAAGPAGKCAAVDVEP
                                                                                                                                                     738 IFSNRGDFRGYCYVEFKEEKSALQALEMDRKSVEGRPMFVSPCVDKSKNPDFKVFRYSTS
                                                                                                                                                                                                                  798 LEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTNRAGKPKGLAYVEYE----NES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKAVKDYICPNIWLEYGQYSVGGIGQKGGLEKVRSVFERALSSVGLHMTKGLALWE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 AKKDFEARMKSFQALQDKFEREKARAKEHQKEIQVLEQRFSDTQLLNLE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U41545; AAK39135.1; -.
WormPep; C02F12.7; CE03901.
Hypothetical protein; Colled coil.
DOMAIN 1279 COLLED COIL (POTENTIAL).
DOMAIN 805 1061 COLLED COIL (POTENTIAL).
SEQUENCE 1130 AA; 131485 WW; BOFDZEFE3D99FB09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 131.5 kDa protein C02F12.7 in chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.3%; Score 216; DB 1;
ilarity 22.0%; Pred. No. 0.00035;
Conservative 123; Mismatches 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                           : | | |:
1879 VKQLKRQLE 1887
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                                                                                                                                                                                                                                                                                                                                          LSLLPRALQ 921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
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hes 172;
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Q11102;
                              623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TEKDSEL-----EXTIAQLEIDNSSKSDQIEKLHLRVNDMLDQMGTIKDEL 771
                                                                                                          MLYTKELEALRDHEEALKEELLARQDEFHDRLQELQLQSKRSREDLV-----SCKN
-OKYIIEIQRLEE----ERKSLRTEKERLGE----TFEMKL---RRAQSLYETELTAAK
                                                                ------DLVLSVHNRAIRNCPW
                                                                                                                                                                                        TVALWSRYLLAMER--HGVDHQVISVTFEKALNAGFIQATDYVEIWQAYLDYLRRRVDFK
                                                                                                                                                                                                                                                                                                                   QDSSKELEELRAAFTRALEYLKQEVEERFNESGDPSCVIMQNWARIEARLCNNMQKAREL
                                                                                                                                                                                                                                                                                                                                                                                ---LRRKARLLTVVEAAKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410 LESVISDLQVEVKALKNKVEFLEKERENLQSQSESQTQLQSSQVDALEAVLHSVTKEKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 TKEHY-EGLLLKERQQA--ESREHAMKKEFSCKLNELEEQYTSLKEELEESARL---DK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523 DELREASEIEIQALRTEKSILAAEIRVLTQKIEDEEQDDITEQLAKIVEDTSQLTRTLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     658 QNVEVAAGPAGKCAAVDVEPPSKQKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSMQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRERI - - - - TGKDA - - EILNLRKOLEKEISHTEDRNRLLHENTQKELE - - - - - - AHKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----EGRPMFVSPCVDK-----SKNPDFKVFRYSTSLEKHKLFISGLPFSCTKEELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            598 AEQRKRARAEKKALKKKKKIRGPEKRGADEDDEKEWGDDEEEQPSKRRRVENSIPAAGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                718 PDTKLRPLFEACGEVVQIRPIFSNRGDFRGYCYVEFKEEKSALQALEMDRKSV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 YPEHVCEVLLTMERTEGSLEDWDIAVQKT-ETRLARVNEQ--RMKAAEKEAALVQQEEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gulli M.-P., Girard J.-P., Zabetakis D., Lapeyre B., Melese T.,
Caizergues-Ferrer M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  680 KHVAENLEAFTS---DKDNLLEELESKNKNIEHLKQEIAQLNEKI----
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842

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REC STRAIN=Berkeley;

REC Addams N. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Addams M.D., Celniker S.E., Holt R.A., Branch R.A., Galle R.F.,

RA Addams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Dony E.E., Downess M., Dugan-Roche S., Dunkov B.C., Dunn P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Cherry J.M., Cawley S., Dahlke C., Devenport L.B., Davies P.,

Burtis K.C., Busam D.A., Butler H., Gu Z., Guan P., Harris M.,

RA Dodgon K., Doup L.E., Downess M., Dugan-Roche S., Dunkov B.C., Dunn P.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moslach J.M.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moslach D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moslach D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moslach D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moslach D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moslach D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moslach D.,

RA Merkulov G., Milshina N.V., Mobarry C., Mo
732 VVQIRPIFSNR-GDFRGYCYVEFKEEKSALQALEMD-RKSVEGRPMFVSPCVDKSKNPDF
                                                                                                                                                                                                              790 KV-----FRYSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVTN-RAGKPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophia melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE-89072740; PubMed-3144044; Robinow S., Campos A.R., Yao K.-M., White K.; Tao R., Yao K.-M., Mite R.; Tao R., Sene product of Drosophila, required in neurons, has three RNP consensus motifs."; Science 242:1570-1572(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elav protein (Embryonic lethal abnormal visual protein).
ELAV OR EG:65F1.2 OR CG4262.
                                                                                                                                                                                                                                                                                                                                                                         409 FGYVTFSDIDSAKKCV-EMNGHFIAGRPCRLDFSTP 443
                                                                                                                                                                                                                                                                                                                                         843 LAYVEYENESQASQAVMKMDGMTIKENIIKVAISNP 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P16914; 09V3F6;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robinow S., Campos A.R., Yao K.-M., White K.; Science 243:12-12(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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ELAV_DROME
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Ray Gouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

Ray Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Ray Collins M., Connor R., Cronin A., Davis P., Feitwell T., Fraser A.,

Rotlins M., Connor R., Cronin N., Harris D., Hidalgo J., Hodgson G.,

Ray Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

Ray James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

Ray Jones L., Jones M., Leather S., McDonald S.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Roddward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

Rabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

Rabel Gen E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Ray Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Ray Lucas A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

Roddinguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

Roddinguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

Roddinguez A., Revuelta D.L., Moreno S., Armstrong J., Forsburg S.L.,

Roddinguez A., Revuelta D.L., Moreno S., Armstrong J., Forsburg S.L.,

Roddinguez A., Revuelta D.L., Moreno S., Armstrong J., Forsburg S.L.,

Roddinguez A., Revuelta D.L., Moreno S., Armstrong J., Forsburg S.L.,

Roddinguez A., Revuelta D.L., Moreno S., Armstrong J., Forsburg S.L.,

Roddinguez R., Revuelta D.L., Moreno S., Armstrong J., Forsburg S.L.,

Roddinguez R., Revuelta D.L., Moreno S., Armstrong S., Marner P.,

Roddinguez R., Revuelta D.L., Jamenez D., Sanchez P.,

Roddinguez R., Revuelta D.L., Moreno S., Armstrong S., Revuelta D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL cutstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        679 S----KQKEKAASLKRDMPKVLHDSSKDS---ITVFVSNLPYSMQEPDTKLRPLFEACGE 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 623 RGADEDDEKEWGDDEEEQ---PSKRRRVENSIPAAGETQNVEVAAGPAGKC-AAVDVEPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 415:871-880(2002).
-!- FUNCTION: HELPS THE ASSEMBLY OF PRE-RIBOSOMAL PARTICLES CONTAINING 18S RRNA.
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PROSITE; PS00030; RRM_RNP_1; 2.
Ribosome biogenesis; RNA-binding; Nuclear protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLUTAR LOCATION: Nuclear; nucleolar.
-1- SIMILARITY: BELONGS TO THE GAR FAMILY.
-1- SIMILARITY: CONTAINS 2 RNA RECGGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> P (IN RÈF. 1).
9D37FAD0C5161A0B CRC64;
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RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76; Mismatches 147;
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                                                                                MEDLINE-21848401; PubMed-11859360;
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HSSP; P11940; 1CVJ.
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SMART; SM00360; RRM; 2.
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341
443
339
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366 4
339 3
500 AA;
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Matches 76; Conserva
                         FROM N.A.
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Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodeg T., Worley K.C., Wu D., Yang S., Yao O.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O., Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                  Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E., Drancell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E., Dranceno S., Gloux S., Lelaure V., Mottler S., Gallbert F., Borkova D. Minana B., Kafatos F.C., Louis C., Siden-Klamos I., Bolshakov S., Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B., Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F., Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., Modillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.2%; Score 210; DB 1; Length 483;
20.9%; Pred. No. 0.00024;
Live 73; Mismatches 135; Indels 140;
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RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
E57336106310810B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AEO03417; AAR45517.1; ALT_INIT. EMBL; AL022139; CAB37430.1; -. PIR, A33130, A33130, A33130, BSPP. P19339; 2SXL. FlyBase; FB90000570; elav. InterPro; IPR002343; Hud_Sxl_RNA. InterPro; IPR000504; RNA_rec_mot. Pfam; PF00076; rrm; 3. PRIWTS; PR00056; RRM; 3. SWART; SW00360; RRM; 3.
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MEDLINE-20196011; Pubmed-10731137;
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PROSITE; PS00030; RRM_RNP_1; 2.
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50817 MW;
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SEQUENCE
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Matches 9
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----NAGSGSQN-----143

122 PQQAQPNTNG---

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675 VEPPSKQKEKAASLKRDMPKVLHDSSKDSITVFVSNLPYSMQEPDTKLRPLFEACGEVVQ 734
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                                                 -----STETRTNLIVNYLPQTMTEDE--IRSLFSSVGEIES
                                                                                                  735 IR-----LEMDRKSVEGRP
                                                                                                                              :: | | | :: | | | :: | 138 VKLIRDKSQVYIDPLNPQAPSKGQSLGYGFVNYVRPQDAEQAVNVLNGLRLQNKII--KV
                                                                                                                                                                                                  775 MFVSPCVDKSKNPDFKVFRYSTSLEKHKLFISGLPFSCTKEELEEICKAHGTVKDLRLVT
                                                                                                                                                                                                                                 835 NRAG--KPKGLAYVEYENESQASQAVMKMDGMTIKE--NIIKVAISNPP-----QRKV
                                                                                                                                                                                                                                                                                                                                                                                                       PE--KPETRKAPGGPMLLPQTYGARGKGRTQLS------LLPRALQRPSAAAPQAEN
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